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OM protein - protein search, using sw model

Run on: December 20, 2004, 14:06:51 ; Search time 153 Seconds
(without alignments)
236.808 Million cell updates/sec

Title: US-10-630-590-288
Perfect score: 528
Sequence: 1 PSELKGFHTTKRKSSRGF.....IGASVDLELCRGYPLEFPDP 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      2002273 begs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :
1: Genesepq.21sep04:*
2: Genesepq.180b:*
3: Genesepq.1990s:*
4: Genesepq.2000a:*
5: Genesepq.2001a:*
6: Genesepq.2002a:*
7: Genesepq.2003a:*
8: Genesepq.2004b:*
9: Genesepq.2004c:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	528	100.0	101	8	ADM53645	Adi53645 Human MAG
2	528	100.0	101	8	ADM33736	Adm33736 Human PDZ1
3	528	100.0	103	7	ADD12353	Add12353 PDZ 11qam
4	528	100.0	104	8	ADD53477	Adi53477 Human PDZ2
5	528	100.0	104	8	ADM33568	Adm33568 Human PDZ3
6	528	100.0	104	8	ADO20999	Ado20999 PDZ domain1
7	528	100.0	108	8	ADM33781	Adm33781 Human PDZ21
8	528	100.0	263	5	ABP63188	Abp63188 Human WWP1
9	515	97.5	99	8	ADIS3658	Adis3658 Human MAG
10	515	97.5	99	8	ADM33749	Adm33749 Human MAG
11	514	97.3	740	5	AAU87919	Aau87919 Human PDZ2
12	485	91.9	94	8	ADIS3657	Adis3657 Human MAG
13	485	91.9	94	8	ADM33748	Adm33748 Human MAG
14	456	86.4	88	8	ADIS3654	Adis3654 Human MAG
15	456	86.4	88	8	ADM33745	Adm33745 Human MAG
16	452	85.6	88	8	ADIS3655	Adis3655 Human MAG
17	452	85.6	88	8	ADM33746	Adm33746 Human MAG
18	436	82.6	85	8	ADIS3652	Adis3652 Human MAG
19	436	82.6	85	8	ADM33743	Adm33743 Human MAG
20	428	81.1	86	5	AAU87854	Aau87854 Human PDZ2
21	418	79.2	887	5	AAU87932	Aau87932 Human PDZ2
22	418	79.2	1112	3	AAB03833	Aab03833 Activin r
23	418	79.2	1161	3	AAB03832	Aab03832 Activin r
24	418	79.2	1216	7	ADD71127	Add71127 Human intrin
25	418	79.2	1277	3	AAB03149	Aab03149 Rat synap

ALIGNMENTS

26	415	78.6	81	8	ADM53656	Adi53656 Human MAG
27	415	78.6	81	8	ADM33747	Adm33747 Human MAG
28	399	75.6	78	8	ADI53653	Adi53653 Human MAG
29	399	75.6	78	8	ADM33744	Adm33744 Human MAG
30	391	74.1	76	8	ADI53651	Adi53651 Human MAG
31	391	74.1	76	8	ADM33742	Adm33742 Human MAG
32	386	73.1	104	8	ADI53366	Adi53366 Human PDZ
33	386	73.1	104	8	ADM33457	Adm33457 Human PDZ
34	379	71.8	103	7	ADI12346	Adi12346 PDZ ligand
35	377	71.4	104	8	ADO20888	PDZ domain
36	367	69.5	72	8	ADI53650	Adi53650 Human MAG
37	367	69.5	72	8	ADM33741	Adm33741 Human MAG
38	365	69.1	72	8	ADI53668	Adi53668 Human MAG
39	365	69.1	72	8	ADI53661	Adi53661 Human MAG
40	365	69.1	72	8	ADM33752	Adm33752 Human MAG
41	365	69.1	72	8	ADM33759	Adm33759 Human MAG
42	364	68.9	72	8	ADI53670	Adi53670 Human MAG
43	364	68.9	72	8	ADI53662	Adi53662 Human MAG
44	364	68.9	72	8	ADI53666	Adi53666 Human MAG
45	364	68.9	72	8	ADI53667	Adi53667 Human MAG

RESULT 1

AD153645	standard; protein; 101 AA.
AD153645;	
22-APR-2004	(first entry)
Human MAGI 1 PDZ domain in pGEX-3X.	
Human; PDZ domain; postsynaptic density-disc-large-20-1; HPV infection; E6 protein; cervical cancer; cytosolic.	
Homo sapiens.	
Synthetic.	
US2004018487-A1.	
29-JAN-2004.	
29-JUL-2003; 2003US-00630590.	
10-NOV-2000; 2000US-00710059.	
16-FEB-2001; 2001US-0269523P.	
03-AUG-2001; 2001US-0309841P.	
19-FEB-2002; 2002US-00080273.	
25-FEB-2002; 2002US-0360061P.	
02-AUG-2002; 2002MO-US924655.	
09-SEP-2002; 2002US-0409298P.	
27-FEB-2003; 2003US-0450464P.	
(LUPS/) LU P S.	
(SCHW/) SCHWEIZER J.	
(DIAZ/) DIAZ-SARMIENTO C S.	
(BELM/) BELMARES M P.	
Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP; WPI; 2004-122015/12.	
Detecting the presence of an oncogenic human papilloma virus (HPV) E6 protein in a sample by contacting a sample suspected of containing an oncogenic HPV E6 protein with a PDZ domain polypeptide.	
Example 4; SEQ ID NO 288; 168pp; English.	
The invention relates to detecting the presence of an oncogenic human papilloma virus (HPV) E6 protein in a sample comprising contacting the	

CC sample with a PDZ domain polypeptide (postsynaptic density, disc-large, CC 20-1) and detecting any binding of the oncogenic HPV E6 protein in the CC sample to the PDZ domain polypeptide. Also included are a system for CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample CC (comprising a first and a second binding partner for an oncogenic HPV E6 CC polypeptide, where the first binding partner is a PDZ domain protein and CC at least one of the binding partners is attached to a solid support, the CC second binding partner being an anti-E6 antibody), determining if a CC subject is infected with an oncogenic strain of HPV and a kit for testing CC for the presence of oncogenic HPV E6 protein (the kit comprising first CC and second binding partners for the oncogenic HPV E6 protein, where the CC first binding partner is a PDZ domain protein). In the method of CC detecting the presence of an oncogenic human papilloma virus (HPV) E6 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is a CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a CC fusion protein with GST (glutathione-S-transferase). The method is a CC performed as part of a test for cervical cancer. The method is useful for CC detecting the presence of an oncogenic human papilloma virus (HPV) E6 CC protein in a sample thereby detecting HPV infection and possible risk of CC cervical cancer. The present sequence is a human PDZ domain in the CC context of its expression as a GST fusion protein.

XX SQ Sequence 101 AA;

Query Match 100.0%; Score 528; DB 8; Length 101;

Best Local Similarity 100.0%; Pred. No. 4.5e-60; Indels 0; Gaps 0;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTHTLKRSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIYSV 60

Db 1 PSELKGFHTHTLKRSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIYSV 60

QY 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPPDP 101

Db 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPPDP 101

RESULT 2

ADM33736 ADM33736 standard; protein; 101 AA.

AC ADM33736;

DT 03-JUN-2004 (first entry)

XX Human PDZ domain #2.

XX human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;

KW Magi-1 PDZ domain 2; human.

XX Homo sapiens.

PN WO2004022006-A2.

XX 18-MAR-2004.

PF 09-SEP-2003; 2003WO-US028508.

PR 09-SEP-2003; 2002US-0409298P.

PR 27-FEB-2003; 2003US-0450464P.

PR 29-JUL-2003; 2003US-00630590.

XX (ARBO-) ARBOR VITA CORP.

PI Lu PS, Schweizer J, Diaz-Sarmiento GS, Belmares MP;

XX WPI, 2004-248368/23.

PT Determining if a human subject is infected with an oncogenic strain of human papillomavirus (HPV) by detecting the presence of any oncogenic HPV

PT E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding partner.

XX Example 4; SEQ ID NO 288; 234pp; English.

XX The invention relates to a method of determining if a human subject is CC infected with an oncogenic strain of human papillomavirus (HPV). CC Determining if a human subject is infected with an oncogenic strain of CC human papillomavirus (HPV) comprises: (1) contacting a sample obtained CC from the subject with a PDZ domain polypeptide bound to a solid support; CC and (2) detecting the presence of any oncogenic HPV E6 protein bound to CC the PDZ domain polypeptide using an HPV E6 binding partner, where the CC presence of oncogenic HPV E6 protein indicates that the subject is CC infected with an oncogenic strain of HPV. The method is performed in CC conjunction with histological analysis of the sample as part of a test CC for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ CC domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18 CC or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is CC directly or indirectly bound to the solid support. The PDZ binding CC partner is a labelled antibody that binds to the oncogenic HPV E6 CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The CC present sequence represents a human PDZ domain used in the method of the CC invention.

XX SQ Sequence 101 AA;

Query Match 100.0%; Score 528; DB 8; Length 101;

Best Local Similarity 100.0%; Pred. No. 4.5e-60; Indels 0; Gaps 0;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTHTLKRSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIYSV 60

Db 1 PSELKGFHTHTLKRSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMKMTGDIYSV 60

QY 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPPDP 101

Db 61 NDTCVLGHHTAQQVVKIPQSIPIGASVDLELCRGYPLPPDP 101

RESULT 3

ADD12353 ADD12353 standard; protein; 103 AA.

AC ADD12353;

DT 01-JAN-2004 (first entry)

XX PDZ ligand (PL) protein #16.

XX modulator; PDZ; post-synaptic density protein 95; PSD95;

KW Drosophila large disc protein; Zonula Occludin 1 protein; ZO-1;

KW PDZ ligand; PL; anti-inflammatory; antiallergic; antitumor; antiproliferative;

KW osteopathic; dermatological; neuroprotective; virucide; antidiabetic;

KW cytosolic; anti-HIV; vasotropic; immunomodulator; neurological disease;

KW immune response disease; muscular disease; cancer;

KW modulating vesicular trafficking; tumour suppression;

KW signal transduction; protein sorting; membrane polarity; apoptosis;

KW synapse formation; multi-protein complex; leukocyte activation inhibitor.

XX Unidentified.

PN WO2003014303-A2.

XX 20-FEB-2003.

PF 02-AUG-2002; 2002WO-US024655.

PR 03-AUG-2001; 2001US-0309841P.

PR 25-FEB-2002; 2002US-0360061P.

XX (ARBO-) ARBOR VITA CORP.

PI Lu PS, Rabinowitz JD, Schweizer J, Carrick DM;
 XX WPI; 2003-268193/26.
 XX
 PT Modulator of binding between discs-large homology repeat protein, PDZ and
 PT PDZ ligand protein, is a peptide having few residues of C-terminal
 PT sequence of PDZ ligand protein.
 XX
 PS Example 7, Page 152; 172pp; English.
 XX
 CC The invention relates to a novel modulator of binding between a PDZ
 CC protein (post-synaptic density protein 95 (PSD95), Drosophila large disc
 CC protein and Zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)
 CC protein. The modulator is a peptide having 3 residues of a C-terminal
 CC sequence of a PL protein. PDZ and PL proteins are a binding pair given in
 CC specification, or a peptide mimetic of the 3 residue PL protein, or a
 CC small molecule having similar functional activity as the 3 residue PL
 CC protein. The reagents of the invention have the following activities:
 CC antiinflammatory, antiallergic, anticancer, antidiabetic, osteopathic,
 CC dermatological, neuroprotective, virucide, antiparasitic, antipneumatic,
 CC antirheumatic, immunosuppressive, antithrombotic, cytostatic, anti-
 CC HIV, vasotropic, and immunomodulator. The novel modulator is useful for
 CC treating a disease correlated with binding between a PDZ protein and PL
 CC protein. The disease can be a neurological disease, immune response
 CC disease, muscular disease or cancer. The modulator is useful for
 CC modulating vesicular trafficking, tumour suppression, signal
 CC transduction, protein sorting, establishment of membrane polarity,
 CC apoptosis, regulation of immune response and organisation of synapse
 CC formation. The modulator is useful for facilitating the assembly of multi-
 CC -protein complexes, often serving as a bridge between several proteins,
 CC or regulating the function of other proteins, and to inhibit leukocyte
 CC activation. The modulator is useful for treating diseases characterised
 CC by inflammatory and humoral immune responses e.g., inflammation, allergy,
 CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,
 CC allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,
 CC diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,
 CC leukemias, infectious diseases (viral infection such as human
 CC immunodeficiency virus (HIV)), and leukaemia. This sequence represents a
 CC PDZ ligand (PL) protein of the invention.
 XX
 SQ Sequence 103 AA;
 CC
 CC Query Match 100.0%; Score 528; DB 7; Length 103;
 CC Best Local Similarity 100.0%; Pred. No. 4.7e-60;
 CC Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 PSELKGFHTTKLRKSSRGFTVVGSDPEDEFLQIKSLVLDGPALDGMETGDIYVSV 60
 CC |||||||
 DB 1 PSELKGFHTTKLRKSSRGFTVVGSDPEDEFLQIKSLVLDGPALDGMETGDIYVSV 60
 CC |||||||
 QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDELICRGYPLPDPD 101
 CC |||||||
 DB 61 NDTCVLGHHTAQQVKIFQSIPIGASVDELICRGYPLPDPD 101
 CC |||||||
 CC
 CC RESULT 4
 CC ADI53477
 CC ID ADI53477 standard; protein; 104 AA.
 CC
 CC ADI53477;
 CC
 CC DT 22-APR-2004 (first entry)
 CC
 CC DE Human PDZ domain for GST fusion protein #120.
 CC
 CC KM Human; PDZ domain; postsynaptic density-disc-large-ZO-1; HPV infection;
 CC KM E6 protein; cervical cancer; cytostatic.
 CC
 CC OS Homo sapiens.
 CC
 CC XX US2004018487-A1.
 CC
 CC XX PD 29-JAN-2004.

XX
 PF 29-JUL-2003; 2003US-00630590.
 XX
 PR 10-NOV-2000; 2000US-00710059.
 PR 16-FEB-2001; 2001US-0269523P.
 PR 03-AUG-2001; 2001US-0209841P.
 PR 19-FEB-2002; 2002US-0080273.
 PR 25-FEB-2002; 2002US-0360061P.
 PR 02-AUG-2002; 2002WO-US024655.
 PR 09-SEP-2002; 2002US-0409298P.
 PR 27-FEB-2003; 2003US-0450464P.
 XX
 PA (LUPS/) LU P S.
 PA (SCHW/) SCHWEIZER J.
 PA (DIAZ/) DIAZ-SARMIENTO C S.
 PA (BELM/) BELMARES M P.
 XX
 PI Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;
 DR WPI; 2004-122015/12.
 XX
 XX Detecting the presence of an oncogenic human papilloma virus (HPV) E6
 PT protein in a sample by contacting a sample suspected of containing an
 PT oncogenic HPV E6 protein with a PDZ domain polypeptide.
 XX
 PS Disclosure; SEQ ID NO 120; 168pp; English.
 XX
 CC The invention relates to detecting the presence of an oncogenic human
 CC papilloma virus (HPV) E6 protein in a sample comprising contacting the
 CC sample with a PDZ domain polypeptide (postsynaptic density, disc-large,
 CC ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the
 CC sample to the PDZ domain polypeptide. Also included are a system for
 CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample
 CC (comprising a first and a second binding partner for an oncogenic HPV E6
 CC polypeptide), where the first binding partner is a PDZ domain protein and
 CC at least one of the binding partners is attached to a solid support, the
 CC second binding partner being an anti-E6 antibody, determining if a
 CC subject is infected with an oncogenic strain of HPV and a kit for testing
 CC for the presence of oncogenic HPV E6 protein (the kit comprising first
 CC and second binding partners for the oncogenic HPV E6 protein, where the
 CC first binding partner is a PDZ domain protein). In the method of
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6
 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids
 CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to
 CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is
 CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a
 CC fusion protein with GST (glutathione-S-transferase). The method is a
 CC performed as part of a test for cervical cancer. The method is useful for
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6
 CC protein in a sample thereby detecting HPV infection and possible risk of
 CC cervical cancer. The present sequence is a human PDZ domain suitable for
 CC inclusion in the test system of the invention.
 CC
 CC XX
 CC
 CC SQ Sequence 104 AA;
 CC
 CC Query Match 100.0%; Score 528; DB 8; Length 104;
 CC Best Local Similarity 100.0%; Pred. No. 4.7e-60;
 CC Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 PSELKGFHTTKLRKSSRGFTVVGSDPEDEFLQIKSLVLDGPALDGMETGDIYVSV 60
 CC |||||||
 DB 1 PSELKGFHTTKLRKSSRGFTVVGSDPEDEFLQIKSLVLDGPALDGMETGDIYVSV 60
 CC |||||||
 QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDELICRGYPLPDPD 101
 CC |||||||
 DB 61 NDTCVLGHHTAQQVKIFQSIPIGASVDELICRGYPLPDPD 101
 CC |||||||
 CC
 CC RESULT 5
 CC ADM33568
 CC ID ADM33568 standard; protein; 104 AA.
 CC
 CC XX ADM33568;
 CC

```
XX 03-JUN-2004 (first entry)
DT Human PDZ domain polypeptide #120.
DE
XX human papillomavirus; HPV, PDZ domain; HPV E6; cervical cancer;
XX Magi-1 PDZ domain 2.
XX Homo sapiens.
OS
XX WO2004022006-A2.
XX 18-MAR-2004.
XX
XX 09-SEP-2003; 2003WO-US028508.
XX
XX 09-SEP-2002; 2002US-0409298P.
XX 27-FEB-2003; 2003US-0450464P.
XX 25-JUL-2003; 2003US-0490094P.
XX 29-JUL-2003; 2003US-00630590.
XX
XX (ARBO-) ARBOR VITA CORP.
XX
XX Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;
XX
XX MPI; 2004-248368/23.
XX
XX Determining if a human subject is infected with an oncogenic strain of
XX human papillomavirus (HPV) by detecting the presence of any oncogenic HPV
XX E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding
XX partner.
XX
XX disclosure; SEQ ID NO 120; 234pp; English.
XX
XX The invention relates to a method of determining if a human subject is
XX infected with an oncogenic strain of human papillomavirus (HPV).
XX Determining if a human subject is infected with an oncogenic strain of
XX human papillomavirus (HPV) comprises: (1) contacting a sample obtained
XX from the subject with a PDZ domain polypeptide bound to a solid support;
XX and (2) detecting the presence of any oncogenic HPV E6 protein bound to
XX the PDZ domain polypeptide using an HPV E6 binding partner, where the
XX presence of oncogenic HPV E6 protein indicates that the subject is
XX infected with an oncogenic strain of HPV. The method is performed in
XX conjunction with histological analysis of the sample as part of a test
XX for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ
XX domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18
XX or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is
XX directly or indirectly bound to the solid support. The PDZ binding
XX partner is a labelled antibody that binds to the oncogenic HPV E6
XX polypeptide. The sample is a cervical scrape, biopsy or lavage. The
XX present sequence represents a PDZ domain polypeptide used in the method
XX of the invention.
XX
XX Sequence 104 AA;
XX
XX Query Match 100.0%; Score 528; DB 8; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 4.7e-60;
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMKMETGDIYSV 60
XX 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMKMETGDIYSV 60
XX
XX 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101
XX 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101
XX
XX DB
XX
XX RESULT 6
XX ADO20999 standard; peptide; 104 AA.
XX
XX ADO20999,
XX AC
```

```
XX 26-AUG-2004 (first entry)
DT PDZ domain polypeptide #120.
DE
XX neuroprotective; gene therapy; N-methyl-D-aspartate receptor;
XX NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;
XX neuronal disorder; stroke; ischaemia; PDZ domain.
XX
XX Unidentified.
XX
XX WO2004045535-A2.
XX
XX 03-JUN-2004.
XX
XX 14-NOV-2003; 2003WO-US036698.
XX
XX 14-NOV-2002; 2002US-0426212P.
XX 14-NOV-2002; 2002US-0426213P.
XX
XX (ARBO-) ARBOR VITA CORP.
XX
XX Lu PS, Garman JD, Belmares MP;
XX
XX MPI; 2004-420526/39.
XX
XX New pharmaceutical composition comprising a polypeptide that inhibits
XX binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein,
XX useful in treating a neuronal disorder e.g. an injury caused by stroke or
XX ischemia.
XX
XX Example 9; Page 120; 146pp; English.
XX
XX The invention describes a pharmaceutical composition comprising an
XX isolated, recombinant or synthetic polypeptide that inhibits binding
XX between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a
XX carrier, diluent or excipient and that comprises a C-terminal amino acid
XX sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated,
XX recombinant or synthetic polypeptide for use in therapy and that
XX comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and
XX inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ
XX protein; and a method for determining whether a test compound inhibits
XX binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.
XX The pharmaceutical composition is useful in treating a neuronal disorder,
XX which is an injury caused by stroke or ischemia. This is the amino acid
XX sequence of a PDZ domain used to produce GST-PDZ fusion proteins.
XX
XX Sequence 104 AA;
XX
XX Query Match 100.0%; Score 528; DB 8; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 4.7e-60;
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMKMETGDIYSV 60
XX 1 PSELKGFHTHTLKRSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMKMETGDIYSV 60
XX
XX 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101
XX 61 NPTCVLGHTHAQVVKIFOSIPIGASVDLELCRGYPLPPDP 101
XX
XX DB
XX
XX RESULT 7
XX ADM33781
XX ID ADM33781 standard; protein; 108 AA.
XX
XX ADM33781;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human PDZ domain/pGEX-3x #3.
XX
XX human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;
XX
```

KM Magi-1 PDZ domain 2; human.
XX Homo sapiens.
OS Synthetic.
XX WO2004022006-A2.
XX 18-MAR-2004.
XX 09-SEP-2003; 2003WO-US028508.
XX 09-SEP-2002; 2002US-0409298P.
XX 27-FEB-2003; 2003US-0450464P.
XX 25-JUL-2003; 2003US-0490094P.
XX 29-JUL-2003; 2003US-00630590.
XX (ARBO-) ARBOR VITA CORP.
XX Lu P8, Schweizer J, Diaz-Sarmiento CS, Belmares MP;
XX WPI; 2004-248368/23.
XX
XX Determining if a human subject is infected with an oncogenic strain of
XX human papillomavirus (HPV) by detecting the presence of any oncogenic HPV
XX E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding
XX partner.
XX
XX Example 4; Page 97; 234pp; English.
XX
XX The invention relates to a method of determining if a human subject is
XX infected with an oncogenic strain of human papillomavirus (HPV).
XX Determining if a human subject is infected with an oncogenic strain of
XX human papillomavirus (HPV) comprises: (1) contacting a sample obtained
XX from the subject with a PDZ domain polypeptide bound to a solid support;
XX and (2) detecting the presence of any oncogenic HPV E6 protein bound to
XX the PDZ domain polypeptide using an HPV E6 binding partner, where the
XX presence of oncogenic HPV E6 protein indicates that the subject is
XX infected with an oncogenic strain of HPV. The method is performed in
XX conjunction with histological analysis of the sample as part of a test
XX for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ
XX domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18
XX or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is
XX directly or indirectly bound to the solid support. The PDZ binding
XX partner is a labelled antibody that binds to the oncogenic HPV E6
XX polypeptide. The sample is a cervical scrape, biopsy or lavage. The
XX present sequence represents a human PDZ domain/pdEx-3X used in the method
XX of the invention.
XX
XX Sequence 108 AA;
XX
XX
XX Query Match 100.0%; Score 528; DB 8; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 5e-60;
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 PSELKKGKFIHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 60
XX 3 PSELKKGKFIHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 62
XX
XX 61 NDTCVLGHHTAQQVVKIFQSIPIGASVDLRCRGYLPFPDD 101
XX 63 NDTCVLGHHTAQQVVKIFQSIPIGASVDLRCRGYLPFPDD 103
XX
XX
XX RESULT 8
XX ABP63188
XX ID ABP63188 standard; peptide; 263 AA.
XX
XX AC ABP63188;
XX
XX
XX 28-OCT-2002 (first entry)
XX
XX Human WMP3 PDZ domain amino acid sequence.
XX
XX

KM Molecular interaction; haematopoietic cell; immune response; T cell;
KM PDZ domain; B cell; endothelial cell; PDZ protein; PSD9; PDZ ligand;
KM Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;
KM immunosuppressive; antiinflammatory; actinallergic; antineuroleptic;
KM anticancer; antiparasitic; dermatological; antiaesthetic; cyostatic;
KM antimicrobial; vasoregic; inflammatory immune response; inflammation;
KM humoral immune response; autoimmune disease; allergy; ulcerative colitis;
KM inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;
KM inflammatory dermatosis; respiratory allergic disease; asthma; cancer;
KM allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;
KM angiogenesis-dependent disorder; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200242422-A2.
XX
XX 30-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US044138.
XX
XX 11-NOV-2000; 2000US-00710059.
XX 24-NOV-2000; 2000US-00721915.
XX 24-NOV-2000; 2000US-00722069.
XX 28-NOV-2000; 2000US-00724553.
XX
XX (ARBO-) ARBOR VITA CORP.
XX
XX Lu P, Rabinowitz JD, Schweizer J;
XX WPI; 2002-608221/65.
XX
XX
XX Modulating the biological function of an endothelial cell or
XX hematopoietic cell e.g., a T-cell or B-cell comprises introducing into
XX the cell, an agent that inhibits binding of a PDZ protein and a PDZ
XX ligand protein in the cell.
XX
XX Disclosure; Page 49-50; 207pp; English.
XX
XX The present invention describes a method (M1) for modulating a biological
XX function of an endothelial cell or haematopoietic cell. M1 comprises
XX introducing into the cell, an agent that inhibits binding of a PDZ
XX (PSD9), Drosophila large disc protein, and Zonula Occludin 1 protein)
XX protein and a PDZ ligand (PL) protein in the cell, and so modulates the
XX biological function. Also described is a method (M2) for determining
XX whether a test compound is an inhibitor of binding between a PDZ protein
XX and a PL protein. M1 is used for modulating a biological function of an
XX endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an
XX inflammatory or humoral immune response, or an autoimmune disease. An
XX inhibitor (I) is useful for treating a disease characterised by leukocyte
XX activation, where the disease is characterised by an inflammatory or
XX humoral immune response, e.g., an autoimmune disease. The compounds e.g.,
XX PI-PDZ interaction inhibitors are useful for treating (ameliorating
XX symptoms of) a variety of diseases and conditions characterised by
XX inflammatory and humoral immune responses e.g., inflammation, allergy,
XX inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,
XX psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic
XX diseases such as asthma, allergic rhinitis, transplantation rejection
XX (cardiac, kidney, liver, small bowel, cornea, pascereis, cadaver,
XX autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,
XX angiogenesis-dependent disorders, infectious diseases and ischaemia.
XX AB096620 to AB096732 and ABP63153 to ABP63578 represent sequences used in
XX the exemplification of the present invention
XX
XX Sequence 263 AA;
XX
XX
XX Query Match 100.0%; Score 528; DB 5; Length 263;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-59;
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 PSELKKGKFIHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 60
XX 1 PSELKKGKFIHTTKRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIVSV 60
XX

CC directly or indirectly bound to the solid support. The PDZ binding
 CC partner is a labelled antibody that binds to the oncogenic HPV E6
 CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The
 CC present sequence represents a human Magi-1 PDZ domain 2 used in the
 CC method of the invention.

SO Sequence 99 AA;

Query Match 97.5%; Score 515; DB 8; Length 99;
 Best Local Similarity 100.0%; Pred. No. 2.1e-58;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SELKGFHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSVN 61
 DB 1 SELKGFHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSVN 60
 QY 62 DTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDDP 100
 DB 61 DTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDDP 99

RESULT 11

AAU87919 standard; protein; 740 AA.

AAU87919;

05-JUN-2002 (first entry)

Human PDZP2 protein.

Human; PDZ domain; MW domain; rat; cow; mouse; fruitfly; protein therapy;
 KM gene therapy; PDZ-mediated disease; inward potassium channel; WBP;
 KM dimer inhibitor peptide; carboxylate binding loop.

Homo sapiens.

MO200207751-A1.

31-JAN-2002.

24-JUL-2001; 2001MO-US023269.

25-JUL-2000; 2000US-0221215P.

28-NOV-2000; 2000US-00723810.

(AXCE-) AXCELL BIOSCIENCES CORP.

Herrero J, Pirozzi G, Uveges A;

WPI; 2002-195842/25.

N-PSDB; ABK46531.

Methods for identifying polypeptides comprising PDZ domains, the
 PT polypeptides and their encoding nucleic acids, useful for the diagnosis
 PT and treatment of PDZ related disorders.

Claim 43; Fig 10; 225pp; English.

The invention relates to methods for identifying polypeptides comprising
 CC PDZ domains, and their encoding nucleic acids. The sequences are used to
 CC identify modulators of their expression, function and activity, for use
 CC in the diagnosis and treatment of PDZ related disorders. Antibodies
 CC against the proteins and cells that produce them may be used for the
 CC treatment of PDZ-mediated disease states. Sequences AAU87919-
 CC represent proteins containing PDZ domains, fragments of these proteins
 CC and other related peptides used in the methods of the invention

Sequence 740 AA;

Query Match 97.3%; Score 514; DB 5; Length 740;
 Best Local Similarity 98.0%; Pred. No. 4.4e-57;
 Matches 99; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSV 60
 DB 128 PSELKGFHTKLRKSRGFGFTVVGSDPEDEFLQIKSLVLDGPAALDGKMETGDIIVSV 187

QY 61 NDTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDDP 101
 DB 188 NDTCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPLPFDDP 228

RESULT 12

AD153657 standard; protein; 94 AA.

AD153657;

22-APR-2004 (first entry)

Human MAGI 1 PDZ domain 2 version 9.

Human; PDZ domain; postsynaptic density-large-20-1; HPV infection;
 KM E6 protein; cervical cancer; cytosolic; MAGI 1.

Homo sapiens.

Synthetic.

US2004018487-A1.

29-JAN-2004.

29-JUL-2003; 2003US-00630590.

10-NOV-2000; 2000US-00710059.

16-FEB-2001; 2001US-0269523P.

03-AUG-2001; 2001US-0309841P.

19-FEB-2002; 2002US-0080273P.

25-FEB-2002; 2002US-0360061P.

02-AUG-2002; 2002MO-US024655.

09-SEP-2002; 2002US-0409298P.

27-FEB-2003; 2003US-0450464P.

(LUPS/) LU P S.

(SCHW/) SCHWEITZER J.

(DIAZ/) DIAZ-SARMIENTO C S.

(BELM/) BELMARES M P.

Lu PS, Schweitzer J, Diaz-Sarmiento CS, Belmares MP;

WPI; 2004-122015/12.

Detecting the presence of an oncogenic human papilloma virus (HPV) E6
 PT protein in a sample by contacting a sample suspected of containing an
 PT oncogenic HPV E6 protein with a PDZ domain polypeptide.

Disclosure; SEQ ID NO 300; 168pp; English.

The invention relates to detecting the presence of an oncogenic human
 CC papilloma virus (HPV) E6 protein in a sample comprising contacting the
 CC sample with a PDZ domain polypeptide (postsynaptic density, disc-large,
 CC ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the
 CC sample to the PDZ domain polypeptide. Also included are a system for
 CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample
 CC (comprising a first and a second binding partner for an oncogenic HPV E6
 CC polypeptide, where the first binding partner is a PDZ domain protein and
 CC at least one of the binding partners is attached to a solid support, the
 CC second binding partner being an anti-E6 antibody), determining if a
 CC subject is infected with an oncogenic strain of HPV and a kit for testing
 CC for the presence of oncogenic HPV E6 protein (the kit comprising first
 CC and second binding partners for the oncogenic HPV E6 protein, where the
 CC first binding partner is a PDZ domain protein). In the method of
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6
 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids
 CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to

CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is
CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a
CC fusion protein with GSR (glutathione-S-transferase). The method is a
CC performed as part of a test for cervical cancer. The method is useful for
CC detecting the presence of an oncogenic human papilloma virus (HPV) E6
CC protein in a sample thereby detecting HPV infection and possible risk of
CC cervical cancer. The present sequence is a PDZ domain from human MAGI 1
CC which may be modified. Note: ADI53650-ADI53687 are listed in the sequence
CC listing and named in table 9, but are not further described in the
CC specification.
XX
SQ Sequence 94 AA;

Query Match 91.9%; Score 485; DB 8; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e-54;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ELKGRFHTKLKRSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 62
DB 1 ELKGRFHTKLKRSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 60
63 TCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPL 96
DB 61 TCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPL 94

RESULT 13
ADM33748 standard; protein; 94 AA.
XX
AC ADM33748;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human Magi-1 PDZ domain 2 #8.
XX
KM human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;
XX Magi-1 PDZ domain 2; human.
XX
OS Homo sapiens.
XX
PN WO2004022006-A2.
XX
PD 18-MAR-2004.
XX
PF 09-SEP-2003; 2003WO-US028508.
XX
PR 09-SEP-2002; 2002US-0409298P.
XX 27-FEB-2003; 2003US-0450464P.
PR 25-JUL-2003; 2003US-0490094P.
PR 29-JUL-2003; 2003US-00630590.
XX
PA (ARBO-) ARBOR VITA CORP.
XX
PI Lu PS, Schweitzer J, Diaz-Sarmiento CS, Belmares MP;
XX WPI; 2004-248368/23.
XX
DR WPI; 2004-248368/23.
XX
PT Determining if a human subject is infected with an oncogenic strain of
PT human papillomavirus (HPV) by detecting the presence of any oncogenic HPV
PT E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding
PT partner.
XX
PS Example 15; SEQ ID NO 300; 234pp; English.
XX
XX The invention relates to a method of determining if a human subject is
CC infected with an oncogenic strain of human papillomavirus (HPV).
CC Determining if a human subject is infected with an oncogenic strain of
CC human papillomavirus (HPV) comprises: (1) contacting a sample obtained
CC from the subject with a PDZ domain polypeptide bound to a solid support;
CC and (2) detecting the presence of any oncogenic HPV E6 protein bound to
CC the PDZ domain polypeptide using an HPV E6 binding partner, where the
CC presence of oncogenic HPV E6 protein indicates that the subject is

CC infected with an oncogenic strain of HPV. The method is performed in
CC conjunction with histological analysis of the sample as part of a test
CC for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ
CC domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18
CC or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is
CC directly or indirectly bound to the solid support. The PDZ binding
CC partner is a labelled antibody that binds to the oncogenic HPV E6
CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The
CC present sequence represents a human Magi-1 PDZ domain 2 used in the
CC method of the invention.
XX
SQ Sequence 94 AA;

Query Match 91.9%; Score 485; DB 8; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e-54;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ELKGRFHTKLKRSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 62
DB 1 ELKGRFHTKLKRSRGFGFTVVGDEPDEFLQISLVLDGPALDGMETGDIYSVND 60
63 TCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPL 96
DB 61 TCVLGHTHAQVVKIFQSIPIGASVDLELCRGYPL 94

RESULT 14
ADI53654 standard; protein; 88 AA.
XX
AC ADI53654;
XX
DT 22-APR-2004 (first entry)
XX
DE Human MAGI 1 PDZ domain 2 version 6.
XX
KM Human; PDZ domain; postnaptic density-large-ZO-1; HPV infection;
XX E6 protein; cervical cancer; cytostatic; MAGI 1.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN US2004018487-A1.
XX
PD 29-JAN-2004.
XX
PF 29-JUL-2003; 2003US-00630590.
XX
PR 10-NOV-2000; 2000US-00710059.
XX 16-FEB-2001; 2001US-0269523P.
PR 03-AUG-2001; 2001US-0309841P.
PR 19-FEB-2002; 2002US-00080273.
XX 25-FEB-2002; 2002US-0360061P.
PR 02-AUG-2002; 2002WO-US024655.
PR 09-SEP-2002; 2002US-0409298P.
XX 27-FEB-2003; 2003US-0450464P.
XX
PA (LUPS/) LU P S.
PA (SCHW/) SCHWEITZER J.
PA (DIAZ/) DIAZ-SARMIENTO C S.
PA (BELM/) BELMARES M P.
XX
PI Lu PS, Schweitzer J, Diaz-Sarmiento CS, Belmares MP;
XX WPI; 2004-122015/12.
XX
DR WPI; 2004-122015/12.
XX
PT Detecting the presence of an oncogenic human papilloma virus (HPV) E6
PT protein in a sample by contacting a sample suspected of containing an
PT oncogenic HPV E6 protein with a PDZ domain polypeptide.
XX
PS Disclosure; SEQ ID NO 297; 168pp; English.
XX
XX The invention relates to detecting the presence of an oncogenic human

CC papilloma virus (HPV) E6 protein in a sample comprising contacting the
 CC sample with a PDZ domain polypeptide (posttranslational density, disc-large,
 CC ZO-1) and detecting any binding of the oncogenic HPV E6 protein in the
 CC sample to the PDZ domain polypeptide. Also included are a system for
 CC detecting the presence of an oncogenic HPV E6 polypeptide in a sample
 CC comprising a first and a second binding partner for an oncogenic HPV E6
 CC polypeptide, where the first binding partner is a PDZ domain protein and
 CC at least one of the binding partners is attached to a solid support, the
 CC second binding partner being an anti-E6 antibody, determining if a
 CC subject is infected with an oncogenic strain of HPV and a kit for testing
 CC for the presence of oncogenic HPV E6 protein (the kit comprising first
 CC and second binding partners for the oncogenic HPV E6 protein, where the
 CC first binding partner is a PDZ domain protein). In the method of
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6
 CC protein in a sample, the PDZ domain polypeptide comprises the amino acids
 CC sequence of human Magi-1 PDZ domain 2. The PDZ domain peptide binds to
 CC HPV E6 protein encoded by HPV strains 16, 18 and 45. The sample is
 CC contacted with multiple PDZ domain polypeptides. The PDZ protein is a
 CC fusion protein with GST (glutathione-S-transferase). The method is a
 CC performed as part of a test for cervical cancer. The method is useful for
 CC detecting the presence of an oncogenic human papilloma virus (HPV) E6
 CC protein in a sample thereby detecting HPV infection and possible risk of
 CC cervical cancer. The present sequence is a PDZ domain from human MAGI 1
 CC which may be modified. Note: AD153650-AD153687 are listed in the sequence
 CC listing and named in table 9, but are not further described in the
 CC specification.

XX SQ Sequence 88 AA;

Query Match Best Local Similarity 100.0%; Pred. No. 8,1e-51; Length 88;

Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FHTKLRKSSRGFGFTVVGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 67
 1 FHTKLRKSSRGFGFTVVGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 60

DB 68 HTHAQVVKIFOSIPIGASVDELRCRGP 95
 61 HTHAQVVKIFOSIPIGASVDELRCRGP 88

RESULT 15

ID ADM33745 standard; protein; 88 AA.

XX AC ADM33745;

DT 03-JUN-2004 (first entry)

XX DE Human Magi-1 PDZ domain 2 #5.

XX KM human papillomavirus; HPV; PDZ domain; HPV E6; cervical cancer;

XX KM Magi-1 PDZ domain 2; human.

OS Homo sapiens.

XX WO2004022006-A2.

XX PD 18-MAR-2004.

XX PF 09-SEP-2003; 2003KO-US028508.

XX PR 09-SEP-2002; 2002US-0409298P.

XX PR 27-FEB-2003; 2003US-0450046P.

XX PR 25-JUL-2003; 2003US-0490094P.

XX PR 29-JUL-2003; 2003US-00630590.

XX PA (ARBO-) ARBOR VITA CORP.

XX PI Lu PS, Schweizer J, Diaz-Sarmiento CS, Belmares MP;

XX WPI, 2004-248366/23.

XX PT Determining if a human subject is infected with an oncogenic strain of
 PT human papillomavirus (HPV) by detecting the presence of any oncogenic HPV
 PT E6 protein bound to the PDZ domain polypeptide using an HPV E6 binding
 PT partner.

XX PS Example 15; SEQ ID NO 297; 234p; English.

XX The invention relates to a method of determining if a human subject is
 CC infected with an oncogenic strain of human papillomavirus (HPV).
 CC Determining if a human subject is infected with an oncogenic strain of
 CC human papillomavirus (HPV) comprises: (1) contacting a sample obtained
 CC from the subject with a PDZ domain polypeptide bound to a solid support;
 CC and (2) detecting the presence of any oncogenic HPV E6 protein bound to
 CC the PDZ domain polypeptide using an HPV E6 binding partner, where the
 CC presence of oncogenic HPV E6 protein indicates that the subject is
 CC infected with an oncogenic strain of HPV. The method is performed in
 CC conjunction with histological analysis of the sample as part of a test
 CC for cervical cancer. The method is an ELISA or a sandwich assay. The PDZ
 CC domain polypeptide binds to HPV E6 protein encoded by HPV strains 16, 18
 CC or 45. It comprises the amino acid sequence of Magi-1 PDZ domain 2. It is
 CC directly or indirectly bound to the solid support. The PDZ binding
 CC partner is a labelled antibody that binds to the oncogenic HPV E6
 CC polypeptide. The sample is a cervical scrape, biopsy or lavage. The
 CC present sequence represents a human Magi-1 PDZ domain 2 used in the
 CC method of the invention.

XX SQ Sequence 88 AA;

Query Match Best Local Similarity 100.0%; Pred. No. 8,1e-51; Length 88;

Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FHTKLRKSSRGFGFTVVGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 67
 1 FHTKLRKSSRGFGFTVVGDEPDEPLQIKSLVLDGPALDGMKMTGDIIVSVNDTCVLG 60

DB 68 HTHAQVVKIFOSIPIGASVDELRCRGP 95
 61 HTHAQVVKIFOSIPIGASVDELRCRGP 88

Search completed: December 20, 2004, 14:18:59
 Job time : 155 secs

STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-09-100-804-23

Query Match 22.1%; Score 116.5; DB 3; Length 79;
Best Local Similarity 40.0%; Pred. No. 7.8e-08;
Matches 26; Conservative 10; Mismatches 24; Indels 5; Gaps 2;

QY 15 KSSRGFTVVG-DEFLQIKSLVLDGPALDGKMETGDIYSVNDTCVLGH 69
DB 1 KNSGIGFSTAGSDNPHIGTDTSTYITKLSGGAADGRSLINDIVSVNDVAVDP 60

QY 70 HAQV 74
DB 61 HAQAV 65

RESULT 3
US-09-290-640-46
Sequence 46, Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcuseon, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 2485
TYPE: PRT
ORGANISM: Homo sapiens
US-09-290-640-46

Query Match 22.0%; Score 116; DB 3; Length 2485;
Best Local Similarity 35.6%; Pred. No. 1.1e-05;
Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

QY 13 LKSSR-GFTVVGDEP--DEFLQIKSLVLDGPALDGKMETGDIYSVNDTCVLGH 68
DB 1096 LKDKATYGLGFOIGKKGRDLGIFISSVAPGADLDGCLKPDRLISVNSVLEGV 1155

QY 69 THAQVVKIFOSIP 81
DB 1156 SHHAILEILQNP 1168

RESULT 4
US-09-665-615B-46
Sequence 46, Application US/09665615B
Patent No. 6653133
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcuseon, Eric G.
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 2485
TYPE: PRT
ORGANISM: Homo sapiens
US-09-665-615B-46

Query Match 22.0%; Score 116; DB 4; Length 2485;
Best Local Similarity 35.6%; Pred. No. 1.1e-05;
Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

QY 13 LKSSR-GFTVVGDEP--DEFLQIKSLVLDGPALDGKMETGDIYSVNDTCVLGH 68
DB 1096 LKDKATYGLGFOIGKKGRDLGIFISSVAPGADLDGCLKPDRLISVNSVLEGV 1155

QY 69 THAQVVKIFOSIP 81
DB 1156 SHHAILEILQNP 1168

RESULT 5
US-09-306-998-3
Sequence 3, Application US/09306998
Patent No. 6291173
GENERAL INFORMATION:
APPLICANT: Bartel, Paul L.
APPLICANT: Tavligian, Sean V.
TITLE OF INVENTION: MMSC2 - An MMAC1 Interacting Protein
FILE REFERENCE: MMSC2
CURRENT APPLICATION NUMBER: US/09/306,998
FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 60/084,740
FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2037
TYPE: PRT
ORGANISM: Homo sapiens
US-09-306-998-3

Query Match 21.1%; Score 111.5; DB 3; Length 2037;
Best Local Similarity 30.2%; Pred. No. 3.4e-05;
Matches 29; Conservative 22; Mismatches 38; Indels 7; Gaps 3;

```

Patent No. 60664472
GENERAL INFORMATION:
APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P. C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-804-3

Query Match 20.9%; Score 110.5; DB 3; Length 2465;
Best Local Similarity 34.7%; Pred. No. 6e-05;
Matches 25; Conservative 17; Mismatches 27; Indels 3; Gaps 2;

Cy 13 LRKSR-GFGFTVGGD--EPDEFLQKSLVLDSPALDGMETGDIYSVNDVCVIGT 69
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1077 LKDKAKTGLGQIRIGGEKMETDGLFISVAPGSPADPHGCLKGRDLISVSVSLGVS 1136
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 70 HAQVVKIFQSIP 81
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1137 HMAAIEILQNP 1148

RESULT 8
US-09-562-737-51
; Sequence 51, Application US/09562737
; Patent No. 6428867
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UMSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737

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CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 51
LENGTH: 206
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-51

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Query Match	20.7%	Score 109.5	DB 4	Length 206
Best Local Similarity	30.1%	Pred. No. 2.5e-06		
Matches 28	Conservative 17	Mismatches 41	Indels 7	Gaps 2

QY 13 LRKSSRGFEFTVGGDE----BEFLQIKSLVLDGPALLDGKMETGDIIVSNPTCVLG 67
Db 77 LTRPDSGLFTNIVGGTDQGVSNDSGIVYSRIKEGGAALADGRLOEGDKILSVNGODLKN 136

QY 68 HTHAQVKKIQQSIPIGASVDLELCRGYPLEFDP 100
Db 137 LLEHDAVDLFRN - AGYAVSLRVQHRLLPVQNGP 167

RESULT 9
US-09-513--999C-7700

Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

```

; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487

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; NUMBER OF SEQ ID NOS: 36681
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; SOFTWARE: Patent.pm
; SEQ ID NO 7700
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: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-513-999C-7700

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Query Match	20.2%	Score 106.5	DB 4	Length 99
Best Local Similarity	31.3%	Pred No. 2.3e-06		
Matches 26	Conservative 17	Mismatches 33	Indels 7	Gaps 2

QY 13 LRKRSRGFGTGVGDEP-----BEFLQIKSLYLDGPALIDGKMGTDVYSVNDTCYLG 67
Db 16 LTRPESGLGPNIVGSTDQQYVSNDSGITVYSRIKENGALLDGRLEGDKTLISVNGDCLKN 75

Qy 68 HTHAQVKKIFQSIPIGASVDLEL 90
| : : : : :
Db 76 LTHQDAVDLFRN--AGYAVSLRV 96

RESULT 10
US-09-270-767-33346

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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

```

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;
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: us/09/270,767
; CURRENT FILING DATE: 1999-03-17
;

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; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 33346
;
; LENGTH: 204
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; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-33346

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Query Match	20.1%	Score 106;	DB 4;	Length 204;
Best Local Similarity	32.8%	Pred. NO. 7.4e-06;		
Matches 22; Conservative	15;	Mismatches 0;	Gaps 0;	

QY 12 KLRKSSKRGFPYVGGDEPDELQIKSLVLDGPALDGMKMGDVIVSNVDTVLGHTHA 71
Db 104 ELPTKEEELGFNNWKGKQNSPIYIISRIIPGVADRRHGLKKGQDLISVNGSVGEENHE 163

Qy	72	QVYKIFQ	78
	:	:	:
Db	164	KAVELLK	170

RESULT 11
US-09-270-767-48563

Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.

FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17

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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48563
LENGTH: 204

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ORGANISM: *Drosophila melanogaster*
US-09-270-767-48563

Best Local Similarity 32.8%; Pred No. 7, 4e-06;
Matches 22; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

Db

104 ELKTEETGLGFNVMMGKESQNSPIYISRIIPGVADRHGGLKRGDQLLSVNGVSEGENHE 163

164 KAVELIK 170

RESULT 12
US-09-151-611-1
; Sequence 1, Application US/09151611

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; GENERAL INFORMATION:
;
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice

```

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; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PP-0599 US
; CURRENT APPLICATION NUMBER: US/09/151.611

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;      NUMBER OF SEQ_ID NOS: 3
;      SOFTWARE: PERL Program
;      SEQ ID NO 1

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; TYPE: prt
; ORGANISM: Homo sapiens
FEATURE: -

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US-09-151-611-1	
Query Match	20.1%; Score 106; DB 2; Length 233;

Query Match	20.14	Score 106	DB 2	Length 233
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Best Local Similarity 32.4%; Pred. No. 8.9e-06;
Matches 22; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 12 KLRKSRGFGFTVGGDEPDEFQIKSLVLDGPALDGMETGDIIVSVNDTCVLGHTHA 71

Db 110 ELPTDEGLGFNNWGGKQNSPIYISRIIPGVAEHRRGGLKRGDQLSVNGSVSGEHHH 169

QY 72 QVVKIFQS 79

Db 170 KAVELLKA 177

RESULT 13

US-09-370-102-1
Sequence 1, Application US/09370102

Patent No. 6255547

GENERAL INFORMATION:

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Patterson, Chandra

TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN

FILE REFERENCE: PF-0599 US

CURRENT APPLICATION NUMBER: US/09/370,102

EARLIER FILING DATE: 1999-08-06

EARLIER APPLICATION NUMBER: 09/151,611

EARLIER FILING DATE: 1998-09-11

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PERL Program

SEQ ID NO 1

LENGTH: 233

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: -

OTHER INFORMATION: 1974337

US-09-370-102-1

Query Match

Best Local Similarity 32.4%; Pred. No. 8.9e-06;
Matches 22; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 12 KLRKSRGFGFTVGGDEPDEFQIKSLVLDGPALDGMETGDIIVSVNDTCVLGHTHA 71

Db 110 ELPTDEGLGFNNWGGKQNSPIYISRIIPGVAEHRRGGLKRGDQLSVNGSVSGEHHH 169

QY 72 QVVKIFQS 79

Db 170 KAVELLKA 177

RESULT 14

US-09-080-855-12
Sequence 12, Application US/09080855A

Patent No. 6083721

GENERAL INFORMATION:

APPLICANT: Sarasz, Jan

APPLICANT: Aspernecm, Pontus

APPLICANT: Heilmann, Ulf

APPLICANT: Gomez, Leonel Jorge

APPLICANT: Heidlin, Carl-Henrik

TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

FILE REFERENCE: 10461/7030

CURRENT APPLICATION NUMBER: US/09/080,855A

EARLIER FILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: 08/805,583

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 2466

TYPE: PRT

ORGANISM: Homo sapiens

US-09-080-855-12

Query Match

Best Local Similarity 32.9%; Pred. No. 0.00033;
Matches 24; Conservative 18; Mismatches 27; Indels 4; Gaps 2;

QY 13 LKRSR-GFGFTVGGDEP---DEFQIKSLVLDGPALDGMETGDIIVSVNDTCVLGH 68

Db 1077 LKDKAKYGLGFQITIGSKMGRDLGIFISSVAPGADPFHGLKPGDRLISVNSVLEGV 1136

QY 69 THAQVVKIFQSIIP 81

Db 1137 SHRAAIEILQNAIP 1149

RESULT 15

US-09-566-076-12
Sequence 12, Application US/09566076

Patent No. 6475775

GENERAL INFORMATION:

APPLICANT: Sarasz, Jan

APPLICANT: Aspernecm, Pontus

APPLICANT: Heilmann, Ulf

APPLICANT: Gomez, Leonel Jorge

APPLICANT: Heidlin, Carl-Henrik

TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

FILE REFERENCE: 10461/7030

CURRENT APPLICATION NUMBER: US/09/566,076

EARLIER FILING DATE: 1998-05-18

EARLIER APPLICATION NUMBER: 09/080,855

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 2466

TYPE: PRT

ORGANISM: Homo sapiens

US-09-566-076-12

Query Match

Best Local Similarity 32.9%; Pred. No. 0.00033;
Matches 24; Conservative 18; Mismatches 27; Indels 4; Gaps 2;

QY 13 LKRSR-GFGFTVGGDEP---DEFQIKSLVLDGPALDGMETGDIIVSVNDTCVLGH 68

Db 1077 LKDKAKYGLGFQITIGSKMGRDLGIFISSVAPGADPFHGLKPGDRLISVNSVLEGV 1136

QY 69 THAQVVKIFQSIIP 81

Db 1137 SHRAAIEILQNAIP 1149

Search completed: December 20, 2004, 14:23:47

Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 14:22:26 ; Search time 146 Seconds
(without alignments)
247.543 Million cell updates/sec

Title: US-10-630-590-288

Perfect score: 528

Sequence: 1 PSLKCKPFIHTLRKSRGF.....IGASVDLELCRGYPDPDP 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppa/PCF_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppa/PCFUS_PUBCOMB.pep:*
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- 9: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/prodata/1/pubppa/US09B_PUBCOMB.pep:*
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- 14: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
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- 18: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	528	100.0	101	US-10-630-590-288	Sequence 288, App
2	528	100.0	101	US-10-789-102-70	Sequence 70, App
3	528	100.0	104	US-10-630-590-120	Sequence 120, App
4	528	100.0	104	US-10-789-102-219	Sequence 219, App
5	515	97.5	99	US-10-630-590-301	Sequence 301, App
6	515	97.5	99	US-10-789-102-328	Sequence 328, App
7	485	91.9	94	US-10-630-590-300	Sequence 300, App
8	485	91.9	94	US-10-789-102-327	Sequence 327, App
9	456	86.4	88	US-10-630-590-297	Sequence 297, App
10	456	86.4	88	US-10-789-102-324	Sequence 324, App
11	452	85.6	88	US-10-630-590-298	Sequence 298, App
12	452	85.6	88	US-10-789-102-325	Sequence 325, App
13	436	82.6	85	US-10-630-590-295	Sequence 295, App

14	436	82.6	85	17	US-10-789-102-322	Sequence 322, App
15	415	78.6	81	15	US-10-630-590-299	Sequence 299, App
16	415	78.6	81	17	US-10-789-102-326	Sequence 326, App
17	399	75.6	78	15	US-10-630-590-296	Sequence 296, App
18	399	75.6	78	17	US-10-789-102-323	Sequence 323, App
19	391	74.1	76	15	US-10-630-590-294	Sequence 294, App
20	391	74.1	76	17	US-10-789-102-321	Sequence 321, App
21	386	73.1	104	15	US-10-630-590-9	Sequence 9, App1
22	386	73.1	104	17	US-10-789-102-108	Sequence 108, App
23	367	69.5	72	15	US-10-630-590-293	Sequence 293, App
24	367	69.5	72	17	US-10-789-102-320	Sequence 320, App
25	365	69.1	72	15	US-10-630-590-304	Sequence 304, App
26	365	69.1	72	15	US-10-630-590-311	Sequence 311, App
27	365	69.1	72	17	US-10-789-102-331	Sequence 331, App
28	365	69.1	72	17	US-10-789-102-338	Sequence 338, App
29	364	68.9	72	15	US-10-630-590-302	Sequence 302, App
30	364	68.9	72	15	US-10-630-590-305	Sequence 305, App
31	364	68.9	72	15	US-10-630-590-306	Sequence 306, App
32	364	68.9	72	15	US-10-630-590-307	Sequence 307, App
33	364	68.9	72	15	US-10-630-590-309	Sequence 309, App
34	364	68.9	72	15	US-10-630-590-310	Sequence 310, App
35	364	68.9	72	15	US-10-630-590-312	Sequence 312, App
36	364	68.9	72	15	US-10-630-590-313	Sequence 313, App
37	364	68.9	72	15	US-10-630-590-321	Sequence 321, App
38	364	68.9	72	15	US-10-789-102-329	Sequence 329, App
39	364	68.9	72	17	US-10-789-102-332	Sequence 332, App
40	364	68.9	72	17	US-10-789-102-333	Sequence 333, App
41	364	68.9	72	17	US-10-789-102-334	Sequence 334, App
42	364	68.9	72	17	US-10-789-102-336	Sequence 336, App
43	364	68.9	72	17	US-10-789-102-337	Sequence 337, App
44	364	68.9	72	17	US-10-789-102-339	Sequence 339, App
45	364	68.9	72	17	US-10-789-102-340	Sequence 340, App

ALIGNMENTS

RESULT 1
US-10-630-590-288
Sequence 288, Application US/10630590
Publicatation No. US20040018487A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter
APPLICANT: Diaz-Sarmiento, Chomorrow Samoza
APPLICANT: Belmonte, Michael P.
TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
FILE REFERENCE: VITA-008
CURRENT APPLICATION NUMBER: US/10/630,590
CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/409,298
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 02/24655
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/080,273
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/269,523
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 09/710,059
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 330
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 288
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-630-590-288

Query Match 100.0%; Score 528; DB 15; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
DB 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60

QY 61 NDTCVLGHHTHAQVVKIFQSIPIGASVDLELCRGYPLPDPD 101
DB 61 NDTCVLGHHTHAQVVKIFQSIPIGASVDLELCRGYPLPDPD 101

RESULT 2
US-10-789-102-70
Sequence 70; Application US/10789102
Publication No. US20040229298A1
GENERAL INFORMATION:
APPLICANT: LU, Peter S
APPLICANT: BAGOWSKI, Christoph Peter
APPLICANT: SCHWEIZER, Johannes
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: Garman, Jonathan David
APPLICANT: BELMARES, MICHAEL P
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
FILE REFERENCE: VITA-009
CURRENT APPLICATION NUMBER: US/10/789,102
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US02/24655
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/080,273
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/269,523
PRIOR FILING DATE: 2002-02-16
PRIOR APPLICATION NUMBER: 09/710,059
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 70
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-789-102-70

Query Match 100.0%; Score 528; DB 17; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
DB 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60

QY 61 NDTCVLGHHTHAQVVKIFQSIPIGASVDLELCRGYPLPDPD 101
DB 61 NDTCVLGHHTHAQVVKIFQSIPIGASVDLELCRGYPLPDPD 101

RESULT 3
US-10-630-590-120
Sequence 120; Application US/10630590
Publication No. US20040018487A1

GENERAL INFORMATION:
APPLICANT: LU, Peter
APPLICANT: SCHWEIZER, Johannes
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: Belmares, Michael P.
TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
FILE REFERENCE: VITA-008
CURRENT APPLICATION NUMBER: US/10/630,590
CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/409,298
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 02/24655
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/080,273
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/269,523
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 09/710,059
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 120
LENGTH: 104
TYPE: PRT
ORGANISM: Homo sapiens
US-10-630-590-120

Query Match 100.0%; Score 528; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60
DB 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYISV 60

QY 61 NDTCVLGHHTHAQVVKIFQSIPIGASVDLELCRGYPLPDPD 101
DB 61 NDTCVLGHHTHAQVVKIFQSIPIGASVDLELCRGYPLPDPD 101

RESULT 4
US-10-789-102-219
Sequence 219; Application US/10789102
Publication No. US20040229298A1
GENERAL INFORMATION:
APPLICANT: LU, Peter S
APPLICANT: BAGOWSKI, Christoph Peter
APPLICANT: SCHWEIZER, Johannes
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: Garman, Jonathan David
APPLICANT: BELMARES, MICHAEL P
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
FILE REFERENCE: VITA-009
CURRENT APPLICATION NUMBER: US/10/789,102
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US02/24655
PRIOR FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/360,061

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; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-102-219
```

```

Query Match          100.0%; Score 528; DB 17; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 PSELKGFIRHTKLKSSRGFGFTVVGDEPDEPLQISLVLDGPAALDGKMETGDIYVSV 60
DB 1 PSELKGFIRHTKLKSSRGFGFTVVGDEPDEPLQISLVLDGPAALDGKMETGDIYVSV 60

QY 61 NDTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGVPLPDPD 101
DB 61 NDTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGVPLPDPD 101
```

```

RESULT 5
US-10-630-590-301
; Sequence 301, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-590-301
```

```

Query Match          97.5%; Score 515; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-55;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 SELKGFIRHTKLKSSRGFGFTVVGDEPDEPLQISLVLDGPAALDGKMETGDIYVSV 61
DB 1 SELKGFIRHTKLKSSRGFGFTVVGDEPDEPLQISLVLDGPAALDGKMETGDIYVSV 60
```

```

QY 62 DTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGVPLPDPD 100
DB 61 DTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGVPLPDPD 99
```

```

RESULT 6
US-10-789-102-328
; Sequence 328, Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Gattan, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-102-328
```

```

Query Match          97.5%; Score 515; DB 17; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-55;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 SELKGFIRHTKLKSSRGFGFTVVGDEPDEPLQISLVLDGPAALDGKMETGDIYVSV 61
DB 1 SELKGFIRHTKLKSSRGFGFTVVGDEPDEPLQISLVLDGPAALDGKMETGDIYVSV 60

QY 62 DTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGVPLPDPD 100
DB 61 DTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGVPLPDPD 99
```

```

RESULT 7
US-10-630-590-300
; Sequence 300, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
```

```

; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-590-300
```

```
Query Match          91.9%; Score 485; DB 15; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 62
          |||
          1 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 60
DB      63 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 96
          |||
          61 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 94
```

```

RESULT 8
US-10-789-102-327
; Sequence 327, Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S
; APPLICANT: BAGOSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORO SOMOZA
; APPLICANT: Garman, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 327
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-102-327
```

```
Query Match          91.9%; Score 485; DB 17; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 62
          |||
          1 ELKGKFIHTKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVND 60
DB      63 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 96
          |||
          61 TCVLGHTHAQVVKIFOSIPIGASVDLELCRGYP 94
```

```

RESULT 9
US-10-630-590-297
; Sequence 297, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Somoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-590-297
```

```
Query Match          86.4%; Score 456; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 8.2e-48;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 FIHTLKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVLG 67
          |||
          1 FIHTLKRSRGFGFTTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVLG 60
DB      68 HTHAQVVKIFOSIPIGASVDLELCRGYP 95
          |||
          61 HTHAQVVKIFOSIPIGASVDLELCRGYP 88
```

```

RESULT 10
US-10-789-102-324
; Sequence 324, Application US/10789102
; Publication No. US20040229298A1
```

```

; GENERAL INFORMATION:
; APPLICANT: LU, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Garman, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CERVICAL CANCER
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 324
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-789-102-324

Query Match      86.4%; Score 456; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 8.2e-48;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FHTRKRSRGFTVVGDEPDEFLQIKSLVLDGPAALDGKMETGDIVSVNDTCVLG 67
DB      1 FHTRKRSRGFTVVGDEPDEFLQIKSLVLDGPAALDGKMETGDIVSVNDTCVLG 60

QY      68 HTHAQQVKIFQSIPIGASVDLELCRGYP 95
DB      61 HTHAQQVKIFQSIPIGASVDLELCRGYP 88

RESULT 11
US-10-630-590-298
; Sequence 298, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: LU, Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
```

```

; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 298
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-630-590-298

Query Match      85.6%; Score 452; DB 15; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e-47;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KGRFHTRKRSRGFTVVGDEPDEFLQIKSLVLDGPAALDGKMETGDIVSVNDTC 64
DB      1 KGRFHTRKRSRGFTVVGDEPDEFLQIKSLVLDGPAALDGKMETGDIVSVNDTC 60

QY      65 VLGHHTHAQQVKIFQSIPIGASVDLELCR 92
DB      61 VLGHHTHAQQVKIFQSIPIGASVDLELCR 88

RESULT 12
US-10-789-102-325
; Sequence 325, Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: LU, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: Garman, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CERVICAL CANCER
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-789-102-325

Query Match      85.6%; Score 452; DB 17; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5e-47;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 KKKFHTKLRKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTC 64
      |||
      1 KKKFHTKLRKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTC 60
      |||

Db      65 VLGHTHAQVVKIFOSIPIGASVDLELCR 92
      |||
      61 VLGHTHAQVVKIFOSIPIGASVDLELCR 88
      |||

RESULT 13
US-10-630-590-295
; Sequence 295, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCES: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 85
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-630-590-295

Query Match      82.6%; Score 436; DB 15; Length 85;
Best Local Similarity 100.0%; Pred. No. 2,2e-45;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FHTKLRKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 67
      |||
      1 FHTKLRKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 60
      |||

Db      68 HTHAQVVKIFOSIPIGASVDLELCR 92
      |||
      61 HTHAQVVKIFOSIPIGASVDLELCR 85
      |||

RESULT 14
US-10-789-102-322
; Sequence 322, Application US/10789102
; Publication No. US20040229298A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S
; APPLICANT: BAGOWSKI, Christoph Peter
; APPLICANT: SCHWEIZER, Johannes
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SONOZA
; APPLICANT: GARMAN, Jonathan David
; APPLICANT: BELMARES, MICHAEL P
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CERVICAL CANCER
```

```
; FILE REFERENCE: VITA-009
; CURRENT APPLICATION NUMBER: US/10/789,102
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2002-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 322
; LENGTH: 85
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-789-102-322

Query Match      82.6%; Score 436; DB 17; Length 85;
Best Local Similarity 100.0%; Pred. No. 2,2e-45;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FHTKLRKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 67
      |||
      1 FHTKLRKSSRGFGFTVGGDEPDEFLQIKSLVLDGPALDGMKMGTVIVSVNDTCVIG 60
      |||

Db      68 HTHAQVVKIFOSIPIGASVDLELCR 92
      |||
      61 HTHAQVVKIFOSIPIGASVDLELCR 85
      |||

RESULT 15
US-10-630-590-299
; Sequence 299, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoza
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
```


SEQ ID NO 299
LENGTH: 81
TYPE: PRT
ORGANISM: Homo sapiens
US-10-630-590-299

Query Match 78.6%; Score 415; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 7,7e-43;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KGKFIHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPPALDGKMETGDIIVSVNDTC 64
DB 1 KGKFIHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPPALDGKMETGDIIVSVNDTC 60
QY 65 VLGHTHAQVVKIFOSIPIGAS 85
DB 61 VLGHTHAQVVKIFOSIPIGAS 81

Search completed: December 20, 2004, 14:34:48
Job time : 147 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 20, 2004, 14:13:02; Search time 38 Seconds

(without alignments)
255.734 Million cell updates/sec

Title: US-10-630-590-288

Perfect score: 528
Sequence: 1 PSELKGRFHTKLRKSSRGF.....IGASVDLELCRGVPLPFDD 101

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	100.0	1171	T42372	probable guanylate
2	528	100.0	1256	JE0209	brain-specific ang
3	418	79.2	1277	T14152	synaptic scaffold
4	242.5	45.9	1012	T23160	hypothetical prote
5	127.5	24.1	1464	T13716	bazooka gene prote
6	121.5	23.0	960	A39651	disce-large tumor
7	121.5	23.0	1337	T13948	atypical protein k
8	116	22.0	2294	T167630	protein-tyrosine-p
9	116	22.0	2466	T167629	protein-tyrosine-p
10	116	22.0	2490	A54971	protein-tyrosine-p
11	115.5	21.9	852	T10811	channel associated
12	115.5	21.9	870	G01974	channel associated
13	114	21.6	2450	S71625	protein-tyrosine-p
14	112.5	21.3	904	I38757	homolog of Drosoph
15	112.5	21.3	926	T13756	homolog of Drosoph
16	110.5	20.9	2054	T46612	multi PDZ domain p
17	110.5	20.9	2055	T30259	multiple PDZ domai
18	109.5	20.7	269	T25079	hypothetical prote
19	109.5	20.7	293	D89193	protein T21C9.1 (l
20	109.5	20.7	2172	T20145	hypothetical prote
21	107.5	20.4	1131	T15617	hypothetical prote
22	106.5	20.2	911	T56552	gammaase-associated
23	105	19.9	1112	T32733	AMPA glutamate rec
24	104.5	19.8	720	A45436	gammaase-associated
25	104.5	19.8	724	JH0800	postsynaptic densi
26	104.5	19.8	767	T09589	postsynaptic densi
27	103	19.5	1944	A59438	KIAA1424 protein (
28	102	19.3	431	T16191	hypothetical prote
29	99	18.8	317	T27179	hypothetical prote

30	98	18.6	628	2	T09458	numb-binding prote
31	98	18.6	728	2	T09457	numb-binding prote
32	97.5	18.5	1666	2	T43169	hypothetical prote
33	96.5	18.3	357	2	S72575	hypothetical prote
34	96.5	18.3	1893	2	A56158	eye development pr
35	93.5	17.7	87	2	S60315	PSD-95-related pro
36	92.5	17.5	117	2	I81209	tyrosine phosphata
37	92.5	17.5	126	2	I81210	tyrosine phosphata
38	92.5	17.5	415	2	UC7167	C kinase 1 interac
39	92.5	17.5	416	2	A56486	perinuclear bindin
40	89	16.9	444	2	T15775	hypothetical prote
41	89	16.9	761	2	T15776	hypothetical prote
42	88	16.7	623	2	A49840	segment polarity p
43	86	16.3	817	2	T03852	protein phosphatase
44	85.5	16.2	352	2	T22159	hypothetical prote
45	85.5	16.2	1252	2	T14272	coractin-binding

ALIGNMENTS

RESULT 1

T42372

probable guanylate kinase (EC 2.7.4.8) 1, membrane-associated, splice form b - mouse

C/Species: Mus musculus (house mouse)

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T42372

R/Dobrosotskaya, I.; Guy, R.K.; James, G.L.

J. Biol. Chem. 272, 31569-31597, 1997

A/Title: MAGI-1, a membrane-associated guanylate kinase with a unique arrangement of pr

A/Reference number: Z22139; PMID:98058950; PMID:9395497

A/Accession: T42372

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-1171 <DOB>

A/Cross-references: UNIPROT:O54893; EMBL:AF027503; NID:g3702346; PID:g3702347; PID:AA

A/Experimental source: strain C57 Black/6 x CBA

C/Genetic:

A/Gene: Magi-1

C/Keywords: alternative splicing; phosphotransferase

F/300-337/Domain: WW repeat homology <MWR1>

F/347-384/Domain: WW repeat homology <MWR2>

Query Match 100.0%; Score 528; DB 2; Length 1171;

Best Local Similarity 100.0%; Pred. No. 3.9e-47;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 PSELKGRFHTKLRKSSRGFTVVGDEPFLQIKSLVLDGPAALDGKMTGDIYSV 60

Db 443 PSELKGRFHTKLRKSSRGFTVVGDEPFLQIKSLVLDGPAALDGKMTGDIYSV 502

QY

61 NDTCVLGHTHAQVVKIFQSIPIGASVDLELCRGVPLPFDD 101

Db 503 NDTCVLGHTHAQVVKIFQSIPIGASVDLELCRGVPLPFDD 543

RESULT 2

JE0209

brain-specific angiogenesis inhibitor-associated protein 1 - human

N/Alternate names: BAI1-associated protein 1; BAP1 [mismomer]

C/Species: Homo sapiens (man)

C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004

C/Accession: JE0209

R/Shizatsuchi, T.; Futamura, M.; Oda, K.; Nishimori, H.; Nakamura, Y.; Tokino, T.

Biochem. Biophys. Res. Commun. 247, 597-604, 1998

A/Title: Cloning and characterization of BAI-associated protein 1: A PDZ domain-contain

A/Reference number: JE0209; PMID:98321173; PMID:9647739

A/Accession: JE0209

A/Molecule type: mRNA

A/Residues: 1-1256 <SHI>

A/Cross-references: UNIPROT:O75085; UNIPROT:Q96QZ7; GB:AB010894; NID:g3370997

A/Experimental source: brain

C/Genetic:

A:Gene: GDB:BAIAP1; BAP1
 A:Cross-references: GDB:9864783
 A:Map position: 3p14.1-3p14.1
 F:300-337/Domain: WW repeat homology <WW1>
 F:359-396/Domain: WW repeat homology <WW2>

Query Match 100.0%; Score 528; DB 2; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 4.2e-47;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60
 DB 463 PSELKGFHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 522

QY 61 NDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 101
 DB 523 NDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 563

RESULT 3

T14152

Synaptic scaffolding protein S-SCAM - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Mar-2004

C:Accession: T14152

R:Hitao, K.; Hata, Y.; Ide, N.; Takeuchi, M.; Irie, M.; Yao, I.; Deguchi, M.; Toyoda, A.

J. Biol. Chem. 273, 21105-21110, 1998

A>Title: A novel multiple PDZ domain-containing molecule interacting with N-methyl-D-aspartate

A:Reference number: Z17889; MUID:98361985; PMID:9694864

A:Accession: T14152

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1277 <HIR>

A:Cross-references: EMBL:AF034863; NID:G3411052; PID:G3411053; PIDN:AA031124.1

C:Genetics:

A:Gene: S-SCAM

C:Function:

A:Description: may assemble receptors and cell adhesion proteins at synaptic junctions

F:302-339/Domain: WW repeat homology <WW1>

F:348-385/Domain: WW repeat homology <WW2>

Query Match 79.2%; Score 418; DB 2; Length 1277;
 Best Local Similarity 74.0%; Pred. No. 1.5e-35;
 Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 2 SELKGFHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 61
 DB 418 SELKGFHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 477

QY 62 DTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 101
 DB 478 DTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 517

RESULT 4
 T23160
 Hypothetical protein K01A6.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T23160
 R:Courtage, A.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: Z19701
 A:Accession: T23160
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1012 <WII>

A:Cross-references: UNIPROT:Q21075; EMBL:Z68750; PIDN:CAA92965.1; GSPDB:GN00022; CESP:K0
 A:Experimental source: clone K01A6
 C:Genetics:
 A:Gene: CESP:K01A6.1
 A:Map position: 4
 A:Introns: 107/1; 151/2; 183/2; 270/2; 316/3; 410/3; 628/3; 922/3; 971/3

F:131-168/Domain: WW repeat homology <WWR>

Query Match 45.9%; Score 242.5; DB 2; Length 1012;
 Best Local Similarity 42.7%; Pred. No. 3e-17;
 Matches 44; Conservative 25; Mismatches 31; Indels 3; Gaps 1;

QY 1 PSELKGFHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 57
 DB 373 PSELKGFHTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 432

QY 58 VSVNDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 100
 DB 433 VSVNDTCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 475

RESULT 5

T13716

bazooka gene protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13716

R:Kuchinke, U.; Grawe, F.; Knust, E.

submitted to the EMBL Data Library, November 1998

A:Description: Control of spindle orientation in Drosophila by the Par-3-related PDZ-dom

A:Reference number: Z17708

A:Accession: T13716

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1464 <KUC>

A:Cross-references: UNIPROT:O96782; EMBL:AJ130871; NID:e1363519; PID:e1363520; PIDN:CA01

C:Genetics:

A:Gene: bazooka

A:Cross-references: FlyBase:FBgn0000163

A:Map position: X

Query Match 24.1%; Score 127.5; DB 2; Length 1464;
 Best Local Similarity 32.3%; Pred. No. 5.5e-05;
 Matches 32; Conservative 19; Mismatches 45; Indels 3; Gaps 1;

QY 6 GKFTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSVND 62
 DB 440 GKFTTKLRKSSRGFGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSVND 499

QY 63 TCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 101
 DB 500 TCVLGHHTAQQVKKIFQSIPIGASVDLELCRGYPLPFDPD 538

RESULT 6
 A39651
 discs-large tumor suppressor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A39651
 R:Woods, D.F.; Bryant, P.J.
 Cell 66, 451-464, 1991
 A>Title: The discs-large tumor suppressor gene of Drosophila encodes a guanylate kinase

A:Reference number: A39651; MUID:91330294; PMID:1651165
 A:Accession: A39651
 A:Molecule type: mRNA
 A:Residues: 1-960 <WOO>
 A:Cross-references: UNIPROT:P31007; GB:M73529; NID:G157243; PIDN:AAA28468.1; PID:G157244
 A:Comment: Loss of this protein causes large imaginal discs by allowing neoplastic overg

rowth to control cellular proliferation.
 C:Genetics:
 A:Gene: FlyBase:d1gl
 A:Cross-references: FlyBase:FBgn0001624
 C:Superfamily: discs-large tumor suppressor; GUGF domain homology; guanylate kinase homc

C:Keywords: signal transduction
 F:45-123/Domain: GUGF domain homology <GUG1>
 F:159-241/Domain: GUGF domain homology <GUG2>
 F:491-563/Domain: GUGF domain homology <GUG3>
 F:607-665/Domain: SH3 homology <SH3>

F:771-948/Domain: guanylate kinase homology <GKI>

Query Match 23.0%; Score 121.5; DB 1; Length 960;

Best Local Similarity 39.7%; Pred. No. 0.00014;

Matches 27; Conservative 11; Mismatches 25; Indels 5; Gaps 2;

12 KLRKSRGFGFTVGG-DEP-DEFLQIKSLVLDGPALDGMKMGTDVIVSVNDTCVL 66

42 QLRKSGGLGFGSTAGTNDHIGTDSITIKLISGAAALDGLRLINDIIVSVNDVSV 101

67 GHTHAQV 74

102 DVEHSAV 109

Db

Db

RESULT 7

atypical protein kinase C isotype-specific interacting protein ASIP - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T13948

R:izum, Y.; Hirose, T.; Tamai, Y.; Hirai, S.; Nagashima, Y.; Fujimoto, T.; Tabuse, Y.;

J. Cell Biol. 143, 95-106, 1998

A:Title: An atypical PKC directly associates and colocalizes at the epithelial tight jun

A:Reference number: 217827; PMID:98437350; PMID:9763423

A/Accession: T13948

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1337 <120>

A/Cross-references: UNIPROT:Q92340; EMBL:AB005549; NID:g3868777; PIDN:BA434216.1; PID:g3

C/Genetics:

A/Gene: abdp

Query Match 23.0%; Score 121.5; DB 2; Length 1337;

Best Local Similarity 28.0%; Pred. No. 0.00021;

Matches 26; Conservative 26; Mismatches 32; Indels 9; Gaps 2;

6 GKFIHTLKRSSRGFTV-----VGDPEDEFLQIKSLVLDGPALDGMKMGTDVIVSV 59

457 GKRLNIQLKKGTGEGFSTSDVTIGGSAP---IYVKNILPRGALIQDGLKAGRLIE 513

60 VNDTCVLGHTHAQVVKIFOSIPGASVDLEICR 92

514 VNGVDLAGKSGEELVSLRSTKMGIVSLVFR 546

Db

RESULT 8

167630

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 -

C/Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C/Accession: 167630

R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.

FEBS Lett. 337, 200-206, 1994

A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane

A:Reference number: 153483; PMID:9411679; PMID:8287977

A/Accession: 167630

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-2294 <RES>

A/Cross-references: UNIPROT:Q12923; GB:D21211; NID:g452193; PIDN:BA04752.1; PID:g452194

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;

C/Keyword: phosphoric monoester hydrolase

F:574-668/Domain: protein 4.1 membrane-binding domain homology <B41>

F:182-1258/Domain: GLGF domain homology <GLG2>

F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 22.0%; Score 116; DB 2; Length 2294;

Best Local Similarity 35.6%; Pred. No. 0.0015;

Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

13 LRKSSR-GFGFTVGGDEP---DEFLQIKSLVLDGPALDGMKMGTDVIVSVNDTCVLGH 68

905 LRKDAKYGFGIIGGKMGRLDGLIFISSVAGPGADLDGLKPGDRLLISVNSVSLGV 964

69 THAQVVKIFOSIP 81

965 SHRAAIEILQNP 977

Db

Db

RESULT 9

167629

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 -

C/Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C/Accession: 167629

R:Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.

FEBS Lett. 337, 200-206, 1994

A:Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran

A:Reference number: 153483; PMID:9411679; PMID:8287977

A/Accession: 167629

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-2466 <RES>

A/Cross-references: UNIPROT:Q12923; GB:D21210; NID:g452191; PIDN:BA04751.1; PID:g45219

C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;

C/Keyword: phosphoric monoester hydrolase

F:574-668/Domain: protein 4.1 membrane-binding domain homology <B41>

F:1354-1430/Domain: GLGF domain homology <GLG2>

F:2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 22.0%; Score 116; DB 2; Length 2466;

Best Local Similarity 35.6%; Pred. No. 0.0016;

Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

13 LRKSSR-GFGFTVGGDEP---DEFLQIKSLVLDGPALDGMKMGTDVIVSVNDTCVLGH 68

1077 LRKDAKYGFGIIGGKMGRLDGLIFISSVAGPGADLDGLKPGDRLLISVNSVSLGV 1136

69 THAQVVKIFOSIP 81

1137 SHRAAIEILQNP 1149

Db

Db

RESULT 10

A54971

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 (

N:Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPp1

C/Species: Homo sapiens (man)

C>Date: 11-Nov-1994 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C/Accession: A54971; A55114; I59595; I53483; S46955

R:Banville, D.; Ahmad, S.; Stocco, R.; Shen, S.H.

J. Biol. Chem. 269, 22320-22327, 1994

A:Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal pr

A:Reference number: A54971; PMID:94350988; PMID:8071359

A/Accession: A54971

A/Molecule type: mRNA

A/Residues: 1-2480 <BAN>

A/Cross-references: UNIPROT:Q12923; GB:U12128

A>Note: sequence shown follows authors' translation at positions 62-63

R:Saras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gomez, L.J.

J. Biol. Chem. 269, 24082-24089, 1994

A:Title: Cloning and characterization of PTP-L1, a protein tyrosine phosphatase with sim

A:Reference number: A55114; PMID:95014139; PMID:7929060

A/Accession: A55114

A/Molecule type: mRNA

A/Residues: 1-61, 'GS', 64-839, 'D', 841-1055, 1075-1133, 'FH', 1136-1210, 'T', 1212-1383, 1389-1

A/Cross-references: GB:X80289; NID:G515030; PIDN:CA56563.1; PID:G515031

R:Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.

Science 268, 411-415, 1995

A:Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.

A:Reference number: I59595; PMID:95232528; PMID:7536343

A/Accession: I59595

A>Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1279-1888 <RES>

A;Cross-references: GB:L34583; NID:g806291; PIDN:AAC41755.1; PID:g806292
 R;Mekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
 FEBS Lett. 337, 200-206, 1994
 A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
 A;Reference number: 153483; MUID:94116679; PMID:8287977
 A;Accession: 153483
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-61, 'GS', 64-839, 'D', 841-1210, 'I', 1212-1383, 1389-2299, 'OM', 2302-2490 <RE2>
 A;Cross-references: GB:D21209; NID:g452189; PIDN:BA04750.1; PID:g452190
 C;Genetics:
 A;Gene: GDB:PTPN13
 A;Cross-references: GDB:306348; OMIM:600267
 A;Map position: 4q21.3-q21.3
 C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
 C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
 F;54-868/Domain: protein 4.1 membrane-binding domain homology <B41>
 F;1099-1175/Domain: GLGF domain homology <GLG1>
 F;1373-1454/Domain: GLGF domain homology <GLG2>
 F;1511-1590/Domain: GLGF domain homology <GLG3>
 F;1799-1870/Domain: GLGF domain homology <GLG4>
 F;1893-1967/Domain: GLGF domain homology <GLG5>
 F;2242-2461/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F;2413/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;2419/Binding site: substrate phosphate (Arg) #status predicted

Query Match 22.0%; Score 116; DB 1; Length 2490;
 Best Local Similarity 35.6%; Pred. No. 0.0016;
 Matches 26; Conservative 18; Mismatches 25; Indels 4; Gaps 2;

OY 13 LRKSR-GFGFTVVGDEP---DEFLQIKSLVDGPALDGMKMTGDIIVSVNDTCVLGH 68
 DB 1096 LKDDAKYGLGFGQIRIGERKMRLDIGIFISVARGPADLDGCLKPGRLISVSVSLGV 1155

OY 69 THAQVVKIPQSIIP 81
 DB 1156 SHRAALEILQNP 1168

RESULT 11
 T10811
 Channel: associated protein of synapse 2 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10811
 R;Irle, M.; Hata, Y.; Takai, Y.
 submitted to the EMBL Data Library, April 1996
 A;Description: Cloning of new isoforms of PSD-95/SAP90 related genes.
 A;Reference number: Z17166
 A;Accession: T10811
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-852 <RT>
 A;Cross-references: UNIPROT:Q63622; EMBL:U53366; NID:g1517939; PID:g1517940
 C;Genetics:
 A;Note: PSD-95/SAP90-related gene 2 (chapsyn isoform2)
 C;Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
 F;198-276/Domain: GLGF domain homology <GLG>
 F;543-601/Domain: SH3 homology <SH3>
 F;663-840/Domain: guanylate kinase homology <GKI>

Query Match 21.9%; Score 115.5; DB 2; Length 852;
 Best Local Similarity 39.1%; Pred. No. 0.00054;
 Matches 27; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

OY 4 LKGRFHTLTKRSSRGFGFTVVGDEPDEFLQIKSLVDGPALDGMKMTGDIIVSVNDT 63
 DB 415 LRGEPRKVLHKSGTGLGFNIVG-EDGEGIFVSLAGPADLSGELGRQQLISVNGI 473
 OY 64 CVLGHHTAQ 72
 DB 474 DLRGASHQ 482

RESULT 12
 G01974
 Channel: associated protein of synapse - human
 C;Species: Homo sapiens (man)
 C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C;Accession: G01974
 R;Kim, E.; Cho, K.
 submitted to the EMBL Data Library, July 1995
 A;Reference number: G08966
 A;Accession: G01974
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-870 <RT>
 A;Cross-references: UNIPROT:Q15700; EMBL:U32376; NID:g1463025; PID:g1036790
 C;Genetics:
 A;Gene: Chapsyn-110
 C;Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase hom
 F;198-276/Domain: GLGF domain homology <GLG2>
 F;543-601/Domain: SH3 homology <SH3>
 F;681-858/Domain: guanylate kinase homology <GKI>

Query Match 21.9%; Score 115.5; DB 2; Length 870;
 Best Local Similarity 39.1%; Pred. No. 0.00055;
 Matches 27; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

OY 4 LKGRFHTLTKRSSRGFGFTVVGDEPDEFLQIKSLVDGPALDGMKMTGDIIVSVNDT 63
 DB 415 LRGEPRKVLHKSGTGLGFNIVG-EDGEGIFVSLAGPADLSGELGRQQLISVNGI 473
 OY 64 CVLGHHTAQ 72
 DB 474 DLRGASHQ 482

RESULT 13
 S71625
 N;Alternate names: epidermal growth factor-binding protein; serine proteinase
 C;Species: Mus musculus (house mouse)
 C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
 C;Accession: S71625; S67987; I81210; I81209; S40290
 R;Chida, D.; Kume, T.; Mukoyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, T.
 FEBS Lett. 358, 233-239, 1995
 A;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very e
 A;Reference number: S71625; MUID:95145716; PMID:7843407
 A;Accession: S71625
 A;Molecule type: mRNA
 A;Residues: 1-2450 <CHI>
 A;Cross-references: UNIPROT:Q64512; UNIPROT:Q62370; EMBL:D83966; NID:g1232103; PIDN:BA1
 A;Experimental source: strain DBA/2; cell line MEL 745A
 R;Wolf, B.B.; Brown, M.D.
 FEBS Lett. 376, 177-180, 1995
 A;Title: Epidermal growth factor-binding protein activates soluble and receptor-bound si
 A;Reference number: S67987; MUID:96105375; PMID:7498536
 A;Accession: S67987
 A;Molecule type: protein
 A;Residues: 1098-1102 <MO>
 A;Experimental source: submaxillary glands
 R;Sato, T.; Irle, S.; Kitada, S.; Reed, J.C.
 Science 268, 411-415, 1995
 A;Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.
 A;Reference number: I59595; MUID:95232528; PMID:7536343
 A;Accession: I81210
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1329-1354, 'K', 1356-1447, 'R', 1449-1454 <RES>
 A;Cross-references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298
 A;Accession: I81209
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1338-1354, 'K', 1356-1447, 'R', 1449-1454 <RE2>
 A;Cross-references: GB:L34581; NID:g806295; PIDN:AAC42055.1; PID:g806296

R; Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
Submitted to the EMBL Data Library, June 1993
A; Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A; Reference number: S40280

A; Accession: S40280
A; Molecule type: mRNA

A; Residues: 2266-2372 <HEN>

A; Cross-references: EMBL:Z23059; NID:G438155; PIDN:CAA80594.1; PID:G438156

C; Geneticks:

A; Gene: Pcpn13

A; Map position: 5

C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C; Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros

F; 566-660/Domain: protein 4.1 membrane-binding domain homology <B41>

F; 1089-1165/Domain: GLGF domain homology <GLG1>

F; 1361-1437/Domain: GLGF domain homology <GLG2>

F; 1495-1574/Domain: GLGF domain homology <GLG3>

F; 1769-1840/Domain: GLGF domain homology <GLG4>

F; 1863-1937/Domain: GLGF domain homology <GLG5>

F; 2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>

F; 2374/Active site: Cys (phosphocysteine intermediate) #status predicted

F; 2380/Binding site: substrate phosphate (Arg) #status predicted

Query Match 21.6%; Score 114; DB 2; Length 2450;
Best Local Similarity 31.4%; Pred. No. 0.0026;

Matches 33; Conservative 17; Mismatches 39; Indels 16; Gaps 3;

Y 2 SELKGRITHTKLKRSRGFTVVGDEPPEFLQIKL-----VLDPALDGMKMTGD 55

Db 1756 SELEVEELLITLVSEKSGSLFTVTKGSG-----SIGCVHVIDDPKAKDRLKAGD 1807

Y 56 VIYSVNDTCVLGHTHAQVVKIFOSIPGASVDLELCRGYPLP 100

Db 1808 RLKVNDDVTVMHTHTDAVNLRAAP--KTVRLVGRILPEKMP 1850

RESULT 14

138757

homolog of Drosophila discs large protein, isoform 1 - human

C; Species: Homo sapiens (man)

C; Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C; Accession: 138757

R; Line, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.

Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994

A; Title: Cloning and characterization of hdig: the human homologue of the Drosophila disc

A; Reference number: 138756; MUID:95024052; PMID:7937897

A; Accession: 138757

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-904 <RES>

A; Cross-references: UNIPROT:Q12959; EMBL:U13897; NID:G558437; PIDN:AAA50599.1; PID:G5584

C; Geneticks:

A; Gene: GDB:DLG1

A; Cross-references: GDB:393278; OMIM:601014

A; Map position: 3q29-3q29

C; Superfamily: disc-large tumor suppressor; GLGF domain homology; guanylate kinase hom

C; Keywords: alternative splicing; duplication

F; 229-307/Domain: GLGF domain homology <GLG1>

F; 324-402/Domain: GLGF domain homology <GLG2>

F; 588-646/Domain: SH3 homology <SH3>

F; 715-892/Domain: guanylate kinase homology <GKI>

Query Match 21.3%; Score 112.5; DB 2; Length 904;

Best Local Similarity 26.5%; Pred. No. 0.0012;

Matches 27; Conservative 20; Mismatches 44; Indels 11; Gaps 2;

Y 7 KFIHTKLKRSRGFTVVG-----DEPPEFLQIKSLVLDGPAALDGMKMTGDIYSVN 61

Db 316 KIMEIKLIKPKGKIGFSIAGVGNHIPPNSIYVTKIIEGAAHKDGLQIGDKLAVN 375

Y 62 DTCVLGHTHAQVVKI-----FOSIPGASVDLELCRGYPLP 97

Db 376 NVCLIEVYTHEAVTALKNTSDFYLVKAKFTSMYNDGYAP 417

RESULT 15

138756

homolog of Drosophila discs large protein, isoform 2 - human

C; Species: Homo sapiens (man)

C; Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C; Accession: 138756

R; Line, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.

Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994

A; Title: Cloning and characterization of hdig: the human homologue of the Drosophila di

A; Reference number: 138756; MUID:95024052; PMID:7937897

A; Accession: 138756

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-926 <RES>

A; Cross-references: UNIPROT:Q12959; EMBL:U13896; NID:G558435; PIDN:AAA50598.1; PID:G558

C; Geneticks:

A; Gene: GDB:DLG1

A; Cross-references: GDB:393278; OMIM:601014

A; Map position: 3q29-3q29

C; Superfamily: disc-large tumor suppressor; GLGF domain homology; guanylate kinase hom

C; Keywords: alternative splicing; duplication

F; 229-307/Domain: GLGF domain homology <GLG1>

F; 324-402/Domain: GLGF domain homology <GLG2>

F; 588-646/Domain: SH3 homology <SH3>

F; 737-914/Domain: guanylate kinase homology <GKI>

Query Match 21.3%; Score 112.5; DB 2; Length 926;
Best Local Similarity 26.5%; Pred. No. 0.0012;

Matches 27; Conservative 20; Mismatches 44; Indels 11; Gaps 2;

Y 7 KFIHTKLKRSRGFTVVG-----DEPPEFLQIKSLVLDGPAALDGMKMTGDIYSVN 61

Db 316 KIMEIKLIKPKGKIGFSIAGVGNHIPPNSIYVTKIIEGAAHKDGLQIGDKLAVN 375

Y 62 DTCVLGHTHAQVVKI-----FOSIPGASVDLELCRGYPLP 97

Db 376 NVCLIEVYTHEAVTALKNTSDFYLVKAKFTSMYNDGYAP 417

Search completed: December 20, 2004, 14:23:00
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 20, 2004, 14:09:42 ; Search time 191 Seconds

(without alignments)
304.256 Million cell updates/sec

Title: US-10-630-590-288

Perfect score: 528

Sequence: 1 PSELKKGKFIHTKLKRSRGF.....IGASVDLELCRGVLPDPDP 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_02:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	100.0	677	2	043863
2	528	100.0	1160	2	096028
3	528	100.0	1171	2	054883
4	528	100.0	1256	2	075085
5	528	100.0	1287	2	096029
6	528	100.0	1462	2	096027
7	528	100.0	1471	2	06RHR9
8	528	100.0	1471	2	AA577818
9	418	79.2	1112	2	AAH59005
10	418	79.2	1252	2	080T00
11	418	79.2	1275	1	AIPI_MOUSE
12	418	79.2	1277	1	AIPI_RAT
13	418	79.2	1455	1	AIPI_HUMAN
14	350	66.3	874	2	09HCD8
15	350	66.3	1074	2	08C0B8
16	350	66.3	1125	2	09H2V6
17	350	66.3	1126	2	09EQJ9
18	346	65.5	1150	2	09HBC4
19	346	65.5	1179	2	09JKT1
20	331.5	62.8	1202	2	09W212
21	315.5	59.8	1057	2	07Q199
22	242.5	45.9	1012	2	021075
23	182	34.5	308	2	09BHW0
24	164	31.1	1027	2	09HIX7
25	149	28.2	266	2	09CR71
26	149	28.2	266	2	09D9V4
27	136	25.8	157	2	07Q462
28	134	25.4	496	2	08CCP7
29	133.5	25.3	1073	2	06GN19
30	130	24.6	409	2	09H5Y8
31	129	24.4	97	2	07Q243

32	127.5	24.1	275	2	09H6Y5
33	127.5	24.1	1464	2	096782
34	126.5	24.0	1464	2	09VX75
35	123.5	23.4	747	2	08IX26
36	123.5	23.4	819	2	08IX28
37	123.5	23.4	943	2	08IX27
38	123.5	23.4	1340	2	06IQ47
39	123.5	23.4	1340	2	AAH71566
40	123.5	23.4	1356	1	PAD3_HUMAN
41	122.5	23.2	200	2	09OX35
42	121.5	23.0	721	2	08BP06
43	121.5	23.0	741	2	08BP04
44	121.5	23.0	816	2	095TF5
45	121.5	23.0	911	2	07KV39

ALIGNMENTS

043863	PRELIMINARY;	PRT;	677 AA.
ID 043863;			
DT 01-JUN-1998 (TREMBLrel. 06, Created)			
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Membrane associated guanylate kinase 1 (Fragment).			
GN Name=MAGI-1;			
OS Homo sapiens (human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=97369492; PubMed=9225980;			
RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,			
RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Rose C.A.;			
RT "cDNA with long CAG trinucleotide repeats from human brain."			
RL Hum. Genet. 100:114-122(1997).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=9833405; PubMed=9647693;			
RA Wood J.D., Yuan J., Margolis R.L., Colomer V., Duan K., Kuehl J.,			
RA Kaminsky Z., Kleiderlein J.J., Sharp A.H., Rose C.A.;			
RT "Atrophin-1, the DRP1A gene product, interacts with two families of WW			
RT domain-containing proteins."			
RL Mol. Cell. Neurosci. 11:149-160(1998).			
CC -1- SIMILARITY: Contains 2 PDZ/DHR domains.			
DR EMBL; U80754; AAC04844.1; -.			
DR HSSP; P46937; 1K9R.			
DR GO; GO:0005911; C:intercellular junction; TAS.			
DR GO; GO:0005886; C:plasma membrane; TAS.			
DR GO; GO:0008022; F:protein C-terminus binding; TAS.			
DR GO; GO:0007155; P:cell adhesion; TAS.			
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.			
DR InterPro; IPR008144; Guanylate_kin.			
DR InterPro; IPR008145; Guanylate_kin.			
DR InterPro; IPR001478; PDZ.			
DR InterPro; IPR001202; WW_Reps_WWP.			
DR Pfam; PF00625; Guanylate_kin1.			
DR Pfam; PF00595; PDZ_2.			
DR Pfam; PF00397; WW_2.			
DR SMART; SM00072; GUKC; 1.			
DR SMART; SM00228; PDZ; 2.			
DR SMART; SM00456; WW; 2.			
DR PROSITE; PSS0052; GUANYLATE_KINASE_2; 1.			
DR PROSITE; PSS0106; PDZ; 2.			
DR PROSITE; PSS0159; WW_DOMAIN_1; 2.			
DR PROSITE; PSS0020; WW_DOMAIN_2; 2.			
KW Kinase.			
FT NON_TER 1 1			
FT NON_TER 677 677			
SEQUENCE 677 AA; 74507 MW; 984C9E8AC49D047 CRC64;			

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Query Match      100.0%; Score 528; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 6,7e-46;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60
    |||||
Db 314 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 373
    |||||

QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 101
    |||||
Db 374 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 414
    |||||

RESULT 2
Q96QZ8 PRELIMINARY; PRT; 1160 AA.
AC Q96QZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DS MAGI-1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laura R.P., Laeky L.A.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 PDZ/DHR domains.
DR EMBL; AF401655; AAK94065.1; -.
DR HSSP; P46937; IK9R.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR008145; Guanylt/Ca.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001202; WW_Reps_WMP.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 4.
DR Pfam; PF00397; WW; 2.
DR SMART; SM00072; GuKC; 1.
DR SMART; SM00228; PDZ; 5.
DR SMART; SM00456; WW; 2.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS01159; WW DOMAIN 1; 2.
DR PROSITE; PS50020; WW DOMAIN 2; 2.
SQ SEQUENCE 1160 AA; 126958 MW; 78PE5B621AC295B0 CRC64;

Query Match      100.0%; Score 528; DB 2; Length 1160;
Best Local Similarity 100.0%; Pred. No. 1.2e-45;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60
    |||||
Db 463 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 522
    |||||

QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 101
    |||||
Db 523 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 563
    |||||

RESULT 3
O54893 PRELIMINARY; PRT; 1171 AA.
AC O54893;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative membrane-associated guanylate kinase 1.
GN Name=Baiapl; Synonyms=Magi-1;
```

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57 Black/6 x CBA;
RC Dobrosotsekaya I.; Guy R.K., James G.L.;
RT "MAGI-1 A Membrane-Associated Guanylate Kinase with a Unique
RT Arrangement of Protein-Protein Interaction Domains.";
RL J. Biol. Chem. 0:0-0(1997).
CC -1- SIMILARITY: Contains 4 PDZ/DHR domains.
DR EMBL; AF027503; AAB91995.1; -.
DR PIR; T42372; T42372.
DR HSSP; P46937; IK9R.
DR WGD; MG1:1203522; Baiapl.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001202; WW_Reps_WMP.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 4.
DR Pfam; PF00397; WW; 2.
DR SMART; SM00072; GuKC; 1.
DR SMART; SM00228; PDZ; 5.
DR SMART; SM00456; WW; 2.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS01159; WW DOMAIN 1; 2.
DR PROSITE; PS50020; WW DOMAIN 2; 2.
SQ SEQUENCE 1171 AA; 127522 MW; FC793D6640D3959 CRC64;

Query Match      100.0%; Score 528; DB 2; Length 1171;
Best Local Similarity 100.0%; Pred. No. 1.2e-45;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 60
    |||||
Db 443 PSELKGFHTKLRKSSRGFTVVGDEPDEFLQIKSLVLDGPALDGMETGDIYSV 502
    |||||

QY 61 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 101
    |||||
Db 503 NDTCVLGHHTAQQVKIFQSIPIGASVDLELCRGYPLPFDPD 543
    |||||

RESULT 4
O75085 PRELIMINARY; PRT; 1256 AA.
AC O75085;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DS BA11-associated protein 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
MEDLINE=98321173; PubMed=9647739;
RA Shiratsuchi T., Futamura M., Oda K., Nishimori H., Nakamura Y.,
RA Tokino T.;
RT "Cloning and characterization of BA1-associated protein 1: a PDZ domain-
RT containing protein that interacts with BA11.";
RL Biochem. Biophys. Res. Commun. 247:597-604(1998).
CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
DR EMBL; AB010894; BAA32002.1; -.
DR PIR; J60209; J60209.
```

DR HSPSP, P46937, 1K9R.
 DR GO:0005515; F:protein binding; IEA.
 DR InterPro: IPR008144; Guanylate_kin.
 DR InterPro: IPR008145; Guanylate_kin.
 DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR001202; WW_Reps_WMP.
 DR Pfam: PF00625; Guanylate_kin; 1.
 DR Pfam: PF00595; PDZ; 5.
 DR Pfam: PF00397; WW; 2.
 DR SMART: SM00072; GUKC; 1.
 DR SMART: SM00228; PDZ; 6.
 DR SMART: SM00456; WW; 2.
 DR PROSITE: PS00856; GUANYLATE_KINASE_1; 1.
 DR PROSITE: PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE: PS50106; PDZ; 6.
 DR PROSITE: PS01159; WW_DOMAIN_1; 2.
 DR PROSITE: PS50020; WW_DOMAIN_2; 2.
 DR PROSITE: PS50020; WW_DOMAIN_2; 2.
 SQ SEQUENCE 1256 AA; 136980 MW; 83PAD2091A4C8E4 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1256;
 Best Local Similarity 100.0%; Pred. No. 1.3e-45;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEDEFLQIKSLVLDGPALDGMKMGTDVIVSV 60
 DB 463 PSELKGFHTKLRKSSRGFTVVGDEDEFLQIKSLVLDGPALDGMKMGTDVIVSV 522

QY 61 NDTCVLGHTHAQVVKIFQSIPIGASVDELICRGYPLPFDD 101
 DB 523 NDTCVLGHTHAQVVKIFQSIPIGASVDELICRGYPLPFDD 563

RESULT 5

Q96QZ9 PRELIMINARY; PRT; 1287 AA.
 AC Q96QZ9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE MAGI-1B alpha beta.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laura R.P., Laesky L.A.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
 DR EMBL: AF401654; AAK94064.1; --
 DR HSPSP, P46937, 1K9R.
 DR GO:0005515; F:protein binding; IEA.
 DR InterPro: IPR008144; Guanylate_kin.
 DR InterPro: IPR008145; Guanylate_kin.
 DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR001202; WW_Reps_WMP.
 DR Pfam: PF00625; Guanylate_kin; 1.
 DR Pfam: PF00595; PDZ; 5.
 DR Pfam: PF00397; WW; 2.
 DR SMART: SM00072; GUKC; 1.
 DR SMART: SM00228; PDZ; 6.
 DR SMART: SM00456; WW; 2.
 DR PROSITE: PS00856; GUANYLATE_KINASE_1; 1.
 DR PROSITE: PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE: PS50106; PDZ; 6.
 DR PROSITE: PS01159; WW_DOMAIN_1; 2.
 DR PROSITE: PS50020; WW_DOMAIN_2; 2.
 SQ SEQUENCE 1287 AA; 140438 MW; C676655657BD5D5 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1287;
 Best Local Similarity 100.0%; Pred. No. 1.4e-45;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEDEFLQIKSLVLDGPALDGMKMGTDVIVSV 60
 DB 463 PSELKGFHTKLRKSSRGFTVVGDEDEFLQIKSLVLDGPALDGMKMGTDVIVSV 522
 QY 61 NDTCVLGHTHAQVVKIFQSIPIGASVDELICRGYPLPFDD 101
 DB 523 NDTCVLGHTHAQVVKIFQSIPIGASVDELICRGYPLPFDD 563

RESULT 6

Q96QZ7 PRELIMINARY; PRT; 1462 AA.
 AC Q96QZ7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE MAGI-1C beta.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laura R.P., Laesky L.A.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
 DR EMBL: AF401656; AAK94066.1; --
 DR PIR: J0209; J0209.
 DR HSPSP, P46937, 1K9R.
 DR Genew: HGNC:946; BA1A1.
 DR GO:0005515; F:protein binding; IPI.
 DR InterPro: IPR008144; Guanylate_kin.
 DR InterPro: IPR008145; Guanylate_kin.
 DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR001202; WW_Reps_WMP.
 DR Pfam: PF00625; Guanylate_kin; 1.
 DR Pfam: PF00595; PDZ; 5.
 DR Pfam: PF00397; WW; 2.
 DR SMART: SM00072; GUKC; 1.
 DR SMART: SM00228; PDZ; 6.
 DR SMART: SM00456; WW; 2.
 DR PROSITE: PS00856; GUANYLATE_KINASE_1; 1.
 DR PROSITE: PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE: PS50106; PDZ; 6.
 DR PROSITE: PS01159; WW_DOMAIN_1; 2.
 DR PROSITE: PS50020; WW_DOMAIN_2; 2.
 SQ SEQUENCE 1462 AA; 161609 MW; 2B98A448A9E7DF89 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1462;
 Best Local Similarity 100.0%; Pred. No. 1.6e-45;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTKLRKSSRGFTVVGDEDEFLQIKSLVLDGPALDGMKMGTDVIVSV 60
 DB 463 PSELKGFHTKLRKSSRGFTVVGDEDEFLQIKSLVLDGPALDGMKMGTDVIVSV 522
 QY 61 NDTCVLGHTHAQVVKIFQSIPIGASVDELICRGYPLPFDD 101
 DB 523 NDTCVLGHTHAQVVKIFQSIPIGASVDELICRGYPLPFDD 563

RESULT 7

Q6RHR9 PRELIMINARY; PRT; 1471 AA.
 AC Q6RHR9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MAGIc alpha beta2 gamma.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=129/SvHe; TISSUE=Brain endothelium;
RA Wegmann F., Ebnet K., Du Pasquier L., Vestweber D., Butz S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
DR EMBL: AY497557; AAS77818.1; --
DR InterPro: IPR008144; Guanylate_kin.
DR InterPro: IPR008145; Guanyl/Ca.
DR InterPro: IPR001202; WW_Reps_WWP.
DR Pfam: PF00625; Guanylate_kin; 1.
DR Pfam: PF00595; PDZ; 5.
DR Pfam: PF00397; WW; 2.
DR SMART: SM00072; GUKC; 1.
DR SMART: SM00456; WW; 2.
DR SMART: SM00428; PDZ; 6.
DR PROSITE: PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE: PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE: PS01159; WW_DOMAIN_1; 2.
DR PROSITE: PS50020; WW_DOMAIN_2; 2.
DR PROSITE: PS01159; WW_DOMAIN_1; 2.
DR PROSITE: PS50020; WW_DOMAIN_2; 2.
SQ SEQUENCE 1471 AA; 161973 MW; 6C780C71CAC37CB1 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1471;
Best Local Similarity 100.0%; Pred. No. 1,6e-45;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSELKGFHTYTKLRKSSRGFGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 60
DB 455 PSELKGFHTYTKLRKSSRGFGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 514
QY 61 NDTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 101
DB 515 NDTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 555

RESULT 8
AAS77818 PRELIMINARY; PRT; 1471 AA.
AC AAS77818;
DT 10-MAY-2004 (TrEMBLrel. 27, Created)
DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE MAGIC alpha beta2 gamma.
GN MAGI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvHe; TISSUE=Brain endothelium;
RA Wegmann F., Ebnet K., Du Pasquier L., Vestweber D., Butz S.;
RL "Endothelial adhesion molecule ESAM binds directly to the multidomain
RT adaptor MAGI-1 and recruits it to cell contacts."
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY497557; AAS77818.1; --
SQ SEQUENCE 1471 AA; 161973 MW; 6C780C71CAC37CB1 CRC64;

Query Match 100.0%; Score 528; DB 2; Length 1471;
Best Local Similarity 100.0%; Pred. No. 1,6e-45;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSELKGFHTYTKLRKSSRGFGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 60
DB 455 PSELKGFHTYTKLRKSSRGFGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 514
QY 61 NDTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 101
DB 515 NDTCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 555

RESULT 9
AAH59005 PRELIMINARY; PRT; 1112 AA.
AC AAH59005;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Activin receptor interacting protein 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedl T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

QY 2 SELKGFHTYTKLRKSSRGFGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 61
DB 254 SOLKGFHTYTKLRKSSRGFGFTVVGDDPDEFLQIKSLVLDGPALDGMETGDIYVSV 313
QY 62 DTCVGLGHHTAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 101
DB 314 EYCVLGHHTAQQVVKIFQSIPIGASVDLELCRGYPLPFPDP 353

RESULT 10
O80TU0 PRELIMINARY; PRT; 1252 AA.
AC O80TU0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKIAA0705 protein (Fragment).
GN Name=Acvripl; Synonyms=mkIAA0705;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22579291; PubMed=12693553;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
 RA Nakajima D., Nagase T., Ohara O., Koga H.,
 RT "Prediction of the coding nucleotide sequences of 400 mouse homologues of KIAA gene:
 RT I. The complete nucleotide sequences of 400 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:35-48(2003).
 CC -1- SIMILARITY: Contains 5 PDZ/DIR domains.
 CC EMBL: AK122349; BAC65631.3; -
 DR MGD; MGI:1354953; Acvrinpl.
 DR GO; GO:0004871; F:signal transducer activity; IPI.
 DR GO; GO:0007165; P:signal transduction; IPI.
 DR InterPro; IPR008145; Guanylate/Ca.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001202; WW_Reps_WWP.
 DR Pfam; PF00397; WW; 2.
 DR Pfam; PF00595; PDZ; 5.
 DR SMART; SM00072; GUKC; 1.
 DR SMART; SM00228; PDZ; 5.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS0106; PDZ; 5.
 DR PROSITE; PS01159; WW_DOMAIN_1; 2.
 DR PROSITE; PS00020; WW_DOMAIN_2; 2.
 FT NON TER 1
 SQ SEQUENCE 1252 AA; 137278 MW; 3D17EBF5918FDC29 CRC64;
 Query Match 79.2%; Score 418; DB 2; Length 1252;
 Best Local Similarity 74.0%; Pred. No. 3.2e-34;
 Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SELKGRIRHRLKSSRGFTVVGDEPPEFLQIKSLVLDGPALDGKRTGVYISVN 61
 DB 263 SOLKGTSLSTLTKKSNMGFTTIGGDEPPEFLQVKSVIPDGPAAODGKRTGVYIYN 322
 QY 62 DTCVLGHTHAOVYKIFOSIPRIGASVDELRCRGYLPDPDP 101
 DB 323 EVCVLGHTHADVYKLFOSVPIGOSVNLVLCRGYLPDPDP 362

RESULT 11
 AIP1_MOUSE STANDARD; PRT: 1275 AA.
 AC Q9WVQ1; O8BYT1; O8CA85;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Atrophin-1 interacting protein 1 (Membrane associated guanylate kinase
 DE Inverted-2) (MGI-2) (Activin receptor interacting protein 1)
 DE (Acvrinpl).
 GN Name=AIP1; Synonyms=Magi2, Atp1, Acvrinpl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10099;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), INTERACTION WITH MADH2, MADH3
 RP AND ACVR2, AND IDENTIFICATION IN A COMPLEX WITH ACVR2, ACVR1B AND
 RP MADH3.
 RC STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE=20148748; PubMed=10681527;
 RA Shoji H., Tsuchida K., Kishi H., Yamakawa N., Matsuzaki T., Liu Z.,
 RA Nakamura T., Sugino H.,
 RT "Identification and characterization of a PDZ protein that interacts
 RT with activin types II receptors.";
 RL J. Biol. Chem. 275:5485-5492(2000).
 RN [2]
 RP SEQUENCE OF 159-112 FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus, and Spinal cord;
 RX MEDLINE=2354683; PubMed=1246885; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Oseko N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schobach C., Gotohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirral L.M., Kanapin A., Matsumura H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad T., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Drigani T.A., Fletcher C.F., Forrest A., Frazier K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Guenrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Megoshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada M.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Walsted C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmfing L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kleikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 CC -1- FUNCTION: Seems to act as scaffold molecule at synaptic junctions
 CC by assembling neurotransmitter receptors and cell adhesion
 CC proteins. May play a role in regulating activin-mediated signaling
 CC in neuronal cells. Enhances the ability of pREN to suppress Akt1
 CC activation (By similarity).
 CC -1- SUBUNIT: Interacts via its WW domains with DRPLA (By similarity).
 CC Interacts via its second PDZ domain with PTEN unphosphorylated C-
 CC terminus (By similarity). Interacts through its guanylate kinase
 CC domain with DLGAP1 (By similarity). Interacts through the PDZ
 CC domains with GRIN2A, GRIN2 and NLGN1 (By similarity). Interacts
 CC with CTNND2, CTNNA1 and MAGIIN-1 (By similarity). Interacts with
 CC ACVR2, MADH2 and MADH3. Part of a complex consisting of AIP1,
 CC ACVR2, ACVR1B and MADH3.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated in synapsesomes (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=long;
 CC Name=2; Synonyms=short;
 CC Name=3; Synonyms=short;
 CC Note=Major;
 CC IsoId=Q9WVQ1-1; Sequence=VSP_008436;
 CC Note=Major;
 CC IsoId=Q9WVQ1-2; Sequence=VSP_008437;
 CC Note=Major;
 CC Note=No experimental confirmation available;
 CC TISSUE SPECIFICITY: Specifically expressed in brain.
 CC -1- SIMILARITY: Belongs to the MAGUK family.
 CC -1- SIMILARITY: Contains 1 guanylate kinase-like domain.
 CC -1- SIMILARITY: Contains 6 PDZ/DIR domains.
 CC -1- SIMILARITY: Contains 5 WW domains.
 CC -1- CAUTION: Ref.2 (BAC29987) sequence differs from that shown due to
 CC a frameshift in position 102.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC DR EMBL; AB029485; BAA82294.1; -
 CC DR EMBL; AK039336; BAC30321.1; ALT INIT.
 CC DR EMBL; AK038407; BAC29987.1; ALT_FRAME.
 CC DR PIR; P70546; P70698.

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DR HSP; P46937; 1K9R.
DR InAcT; Q9WV01; -.
DR MGB; MGI:1354953; Acvtr1npl.
DR GO; GO:0004871; P:signal transducer activity; IPT.
DR GO; GO:0007165; P:signal transduction; IPT.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR008145; Guanylt/Ca.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001202; WW_Reps_WMP.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00585; PDZ; 6.
DR Pfam; PF00397; WW; 2.
DR SMART; SM00072; Gukc; 1.
DR SMART; SM00228; PDZ; 6.
DR SMART; SM00456; WW; 2.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS50106; PDZ; 6.
DR PROSITE; PS01159; WW_DOMAIN_1; 2.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
DR PROSITE; PS01159; WW_DOMAIN_1; 2.
DR PROSITE; PS50020; WW_DOMAIN_2; 2.
DR Alternative splicing; Repeat.
KW DOMAIN 17 101 PDZ 1.
FT DOMAIN 109 285 Guanylate_kinase.
FT DOMAIN 301 334 WW 1.
FT DOMAIN 347 380 WW 2.
FT DOMAIN 425 509 PDZ 2.
FT DOMAIN 604 682 PDZ 3.
FT DOMAIN 777 859 PDZ 4.
FT DOMAIN 919 1009 PDZ 5.
FT DOMAIN 1139 1221 PDZ 6.
FT VARSPLIC 1 163 Missing (in isoform 2).
FT VARSPLIC 1229 1275 /FtId=VSP_008436.
FT FT MPSSLSMKCKSDKSGSPYFLGHPKDTNTPRGVLPPLP
FT FT PDCRK -> AFHSPFLCASFVF (in isoform 3).
SQ SEQUENCE 1275 AA; 140918 MW; F1YDC52517806354 CRC64;

Query Match 79.2%; Score 418; DB 1; Length 1275;
Best Local Similarity 74.0%; Pred. No. 3.3e-34;
Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 2 SEIKGRFHTKTKRKSSRGFFTVVGGDEPDEPLQIKSLVLDGPAALDGKMTGDIIVSYN 61
DB 417 SOLKGFELSTLTKSKMNGFFITIGDEPDEPLQVKSVPIDGPAADGKMTGDIIVSYN 61
QY 62 DTCVLGHTAQQVVKIRFOSIPFGASVDELRCRGPLPPDP 101
DB 477 EVCVLGHTHADVVKLFQSVPLIGOSVNLVLCRGYPLPPDP 516

RESULT 12
AIP1_RAT STANDARD; PRT; 1277 AA.
AC 088382; Q9R271;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Atrophin-1 interacting protein 1 (Membrane associated guanylate kinase
inverted-2) (MAGI-2) (Synaptic scaffolding molecule) (S-SCAM).
GN Name=Aip1; Synonyms=Meg12, Secam;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, SUBCELLULAR LOCATION, TISSUE
SPECIFICITY, AND INTERACTION WITH DLGAP1, NLGN1 AND GRIN2A.
RX MEDLINE=98361985; PubMed=9694864;
RA Hirao K., Hata Y., Ide N., Takeuchi M., Irie M., Yao I., Deguchi M.,
RA Toyoda A., Suehosh T.C., Takai Y.;
RA "A novel multiple PDZ domain-containing molecule interacting with N-
methyl-D-aspartate receptors and neuronal cell adhesion proteins.";
RL J. Biol. Chem. 273:21105-21110(1998).

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RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND ALTERNATIVE SPLICING (ISOFORM 3).
RX MEDLINE=20112872; PubMed=10644767;
RA Hirao K., Hata Y., Yao I., Deguchi M., Kawabe H., Mizoguchi A.,
RA Takai Y.;
RA "three isoforms of synaptic scaffolding molecule and their
characterization: multimerization between the isoforms and their
RT interaction with N-methyl-D-aspartate receptors and SAP90/PSD-95-
associated protein."
RL J. Biol. Chem. 275:2966-2972(2000).
RN [3]
RP INTERACTION WITH MAGUIN-1.
RX MEDLINE=99223514; PubMed=10207009;
RA Yao I., Hata Y., Ide N., Hirao K., Deguchi M., Nishio H.,
RA Mizoguchi A., Takai Y.;
RA "MAGUIN, a novel neuronal membrane-associated guanylate kinase-
interacting protein."
RL J. Biol. Chem. 274:11889-11896(1999).
RN [4]
RP INTERACTION WITH CTNND2.
RX MEDLINE=99182311; PubMed=10080919; DOI=10.1006/brc.1999.0364;
RA Ide N., Hata Y., Deguchi M., Hirao K., Yao I., Takai Y.;
RA "interaction of S-SCAM with neuronal plakophilin-related Armadillo-
repeat protein/delta-catenin."
RL Biochem. Biophys. Res. Commun. 256:456-461(1999).
RN [5]
RP INTERACTION WITH GRID2.
RX MEDLINE=22477859; PubMed=12589829; DOI=10.1016/S0006-291X(03)00070-6;
RA Yap C.C., Muto Y., Kishida H., Hashikawa T., Yano R.;
RA "PKC regulates the delta2 glutamate receptor interaction with S-
SCAM/MAGI-2 protein."
RL Biochem. Biophys. Res. Commun. 301:1122-1128(2003).
RN [6]
RP FUNCTION: Seems to act as scaffold molecule at synaptic junctions
by assembling neurotransmitter receptors and cell adhesion
proteins. May play a role in regulating activin-mediated signaling
in neuronal cells. Enhances the ability of PTEN to suppress Akt1
activation (By similarity).
CC -! SUBUNIT: Interacts through the PDZ domains its with
DLGAP1. Interacts with CTNND2 and MAGUIN-1. Interacts with CTNBL1,
NLGN1, MADH2 and MADH3 (By similarity). Part of a complex
consisting of AIP1, ACVR2, ACVR1B and MADH3 (By similarity).
interacts via its WW domains with DRP1A (By similarity). Interacts
via its second PDZ domain with PTEN unphosphorylated C-terminus
(BY similarity)
CC -! SUBCELLULAR LOCATION: Membrane-associated in synapsesomes.
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=alpha;
CC IsoId=088382-1; Sequence=Displayed;
CC Name=2; Synonyms=beta;
CC IsoId=088382-2; Sequence=VSP_008438;
CC Name=3; Synonyms=gamma;
CC IsoId=088382-3; Sequence=VSP_008439;
CC -! TISSUE SPECIFICITY: Exclusively expressed in brain.
CC -! SIMILARITY: Belongs to the MAGUK family.
CC -! SIMILARITY: Contains 1 guanylate kinase-like domain.
CC -! SIMILARITY: Contains 6 PDZ/DHR domains.
CC -! SIMILARITY: Contains 2 WW domains.
CC -----
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or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL; AF038663; AAC31122.1; -
DR EMBL; AF130819; AAD31015.1; -
DR HSP; P46937; 1K9R.
DR InterPro; IPR008144; Guanylate_kin.
DR InterPro; IPR008145; Guanylt/Ca.

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DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001202; WW_Rap5_WMP.
 DR Pfam; PF00652; Guanylate_kin_1.
 DR Pfam; PF00595; PDZ; 6.
 DR Pfam; PF00397; WW; 2.
 DR SMART; SM00072; Gukc; 1.
 DR SMART; SM00228; PDZ; 6.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
 DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE; PS50106; PDZ; 6.
 DR PROSITE; PS01159; WW_DOMAIN_1; 2.
 DR PROSITE; PS50020; WW_DOMAIN_2; 2.
 KM Alternative splicing; Repeat.
 FT DOMAIN 17 101 PDZ.
 FT DOMAIN 109 285 Guanylate kinase.
 FT DOMAIN 302 335 WW 1.
 FT DOMAIN 348 381 WW 2.
 FT DOMAIN 426 510 PDZ 1.
 FT DOMAIN 605 683 PDZ 2.
 FT DOMAIN 778 860 PDZ 3.
 FT DOMAIN 920 1010 PDZ 4.
 FT DOMAIN 1141 1223 PDZ 5.
 FT VARSPLIC 1 163 Missing (in isoform 2).
 FT VARSPLIC 1 223 Missing (in isoform 3).
 FT VARSPLIC 1 223 Missing (in isoform 3).
 FT CONFLICT 645 645 L -> F (in Ref. 2).
 FT SEQUENCE 1277 AA; 141071 MW; E1A435F35549DF9 CRC64;
 Query Match 79.2%; Score 418; DB 1; Length 1277;
 Best Local Similarity 74.0%; Pred. No. 3.3e-34;
 Matches 74; Conservative 15; Mismatches 11; Indels 0; Gaps 0;
 QY 2 SELKGFHTLRKSSRGFGFTVVGSDPEFLQIKSLVLDGPAALDGMKGTGVISVN 61
 DB 418 SOLKGFHTLRKSSRGFGFTVVGSDPEFLQIKSLVLDGPAALDGMKGTGVISVN 61
 QY 62 DTCTVLTHTAQQVYKFGSIPRIGASVDLELCGYPLRPDP 101
 DB 478 EVCVLGHTHADVNTLFGSVPFGDSVNLVLCRGYPLRPDP 517

RESULT 13
 AIP1_HUMAN STANDARD; PRT; 1455 AA.
 ID AIP1_HUMAN
 AC Q86UL8; O60434; O60510; Q86UL7; Q9UD05; Q9UDU1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Atrophin-1 interacting protein 1 (Atrophin-1 interacting protein A)
 DE Membrane associated guanylate kinase Inverted-2 (MAGI-2).
 OS Homo sapiens (Human).
 GN Name=AIP1; Synonym=Magi2; KIAA0705;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND INTERACTION
 RP WITH DRPLA.
 RC TISSUE=Brain;
 RX MEDLINE=88333405; PubMed=8647693;
 RA Wood J.D., Yuan J., Margolis R.L., Colomer V., Duan K., Kushi J.,
 RA Kaminsky Z., Kleiderlein J.J., Sharp A.H., Ross C.A.;
 RT "Atrophin-1, the DRPLA gene product, interacts with two families of WW
 RL domain-containing proteins.";
 RL Mol. Cell. Neurosci. 11:149-160(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=88403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 RN [3]
 RP SEQUENCE OF 1-100; 141-179; 350-682; 684-1175 AND 1237-1455 FROM N.A.
 RA Courtney L., Harrison M., Lemox S., Bourne S., Ozereky P., Carter T.,
 RA Tin-Molam A., Hawkins M., Keppler D., Sulston J.E., Eldred J.,
 RA Kozlowicz A., Bemis G., Langston Y., Mead K., Haakenon W., Meyer R.,
 RA Shih K., Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH PTEN.
 RX MEDLINE=20226087; PubMed=10760291;
 RA Wu X., Hegner K., Castellano-Prabhu S., Do D., Kaye M.B., Yuan X.-J.,
 RA Wood J., Ross C., Sawyers C.L., Wang Y.E.;
 RT "Evidence for regulation of the PTEN tumor suppressor by a membrane-
 RL localized multi-PDZ domain containing scaffold protein MAGI-2.";
 RN Proc. Natl. Acad. Sci. U.S.A. 97:4233-4238(2000).
 RN [5]
 RP INTERACTION WITH PTEN.
 RX MEDLINE=21623681; PubMed=11707428; DOI=10.1074/jbc.C100556200;
 RA Vazquez F., Grossman S.R., Takahashi Y., Rokae M.V., Nakamura N.,
 RA Sellers W.R.;
 RT "Phosphorylation of the PTEN tail acts as an inhibitory switch by
 RL preventing its recruitment into a protein complex.";
 RL J. Biol. Chem. 276:48627-48630(2001).
 CC -1- FUNCTION: Seems to act as scaffold molecule at synaptic junctions
 CC by assembling neurotransmitter receptors and cell adhesion
 CC proteins. May play a role in regulating activin-mediated signaling
 CC in neuronal cells. Enhances the ability of PTEN to suppress AKT1
 CC activation.
 CC -1- SUBUNIT: Interacts via its WW domains with DRPLA. Interacts via
 CC its second PDZ domain with PTEN unphosphorylated C-terminus.
 CC Interacts through its guanylate kinase domain with DLGAP1 (By
 CC similarity). Interacts through the PDZ domains with GRIN2A, GRIN2
 CC and NUGN1 (By similarity). Interacts with CTNND2, CTNNA1, MAGUIN-
 CC 1, ACVR2, MADH2 and MADH3 (By similarity). Part of a complex
 CC consisting of AIP1, ACVR2, ACVR1B and MADH3 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated in synaptosomes (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q86UL8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q86UL8-2; Sequence=VSP_008435;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Specifically expressed in brain.
 CC -1- SIMILARITY: Belongs to the MAGUK family.
 CC -1- SIMILARITY: Contains 1 guanylate kinase-like domain.
 CC -1- SIMILARITY: Contains 6 PDZ/DHR domains.
 CC -1- SIMILARITY: Contains 2 WW domains.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF038563; AAC05370.1; -
 CC EMBL; AB014605; BA31680.2; ALT_INT.
 CC EMBL; AC004808; AAC23438.1; -
 CC EMBL; AC004945; AAC61488.1; -
 CC EMBL; AC004990; AAC79151.1; -
 CC EMBL; AC005246; AAC25530.1; -
 CC EMBL; AC006043; AAD15413.2; -
 CC EMBL; AC007320; AAP22360.1; -
 CC EMBL; AC007337; AAP21886.1; -
 CC PDB; 1UBP; NMR; A=768-873.
 CC PDB; 1UBO; NMR; A=405-526.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20450683; PubMed=10997877;
 RA Nagase T., Kikuno R., Nakayama M., Hiroseawa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes.
 RT XVII. The complete sequences of 100 new cDNA clones from brain which
 RT code for large proteins in vitro."
 RL DNA Res. 7:273-281(2000).
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
 DR EMBL; AB046854; BAB13460.1; -
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001202; WW_Rsp5_WMP.
 DR Pfam; PF00555; PDZ; 5.
 DR Pfam; PF00397; WW; 2.
 DR SMART; SM00228; PDZ; 5.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PSS0106; PDZ; 5.
 DR PROSITE; PSS0159; WW_DOMAIN 1; 2.
 DR PROSITE; PSS0020; WW_DOMAIN 2; 2.
 RT NON TER 1
 SQ SEQUENCE 874 AA; 95522 MW; 32CBDD7CE59838A CRC64;
 Query Match 66.3%; Score 350; DB 2; Length 874;
 Best Local Similarity 60.4%; Pred. No. 2,4e-27;
 Matches 61; Conservative 18; Mismatches 22; Indels 0; Gaps 0
 Oy 1 PSELKGFHTHTKLRSSRGFGPTVVGGDEDFLOIKSLVLDGPAALDGKRETDVIVSV 60
 Db 150 PSOLKGLVRLASIKSTMGFTITIGCRPDEFLLQKVVLLXDPAAOGKIALPDVYDI 209
 Oy 61 NDTCVLGHHTAQQVAKIFQSIPIGASVDELCEGYLPPDDP 101
 Db 210 NGNCVLGHTHADVQMFQVLPVNOYVNLTLRCGYLPPDSE 250
 RESULT 15
 OS O8COP8 PRELIMINARY; PRT; 1074 AA.
 AC O8COP8;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:49322436K10 product:MEMBRANE-ASSOCIATED GUANYLATE
 DE KINASE-RELATED MAGI-3 homolog (Fragment).
 GN Name=6530407C02RLK;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=99279253; PubMed=10349636;
 RX KA Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning."
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=21085660; PubMed=11217851;
 RX RIKEN FANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT Nature 420:563-573(2002).
 RL

RP [4] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=204939374; PubMed=110422159,
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.,"
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076661;
 RA Shibata K., Itoh M., Arakawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuwa T., Teshiro H., Itoh M.,
 RA Sun H., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiyake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated resource analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.,"
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adechi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirao T., Hirozane W.,
 RA Kuroda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Horii F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kanakawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kiyohara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sekai C., Sekai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Tuya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JULY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 - SIMILARITY: Contains 4 PDZ/DHR domains.
 EMBL: AK030063; BAC26773.1; -.
 DR HSSP; P46937; IKR9.
 DR WGD; MG1:1923484; 6530407C02R1K.
 DR GO; GO:0016301; P:kinase activity; IEA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR008144; Guanylate_kin.
 DR InterPro; IPR009145; Guanylt/Ca.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001202; WW_Rpds_WWP.
 DR Pfam; PF006925; Guanylate_kin; 1.
 DR Pfam; PF00397; WW; 2.
 DR Pfam; PF000072; Gukc; 1.
 DR SMART; SM00228; PDZ; 6.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
 DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
 DR PROSITE; PS50106; PDZ; 6.
 DR PROSITE; PS01159; WW_DOMAIN_1; 2.
 DR PROSITE; PS50020; WW_DOMAIN_2; 2.
 KW Kinase.
 PT NON TER 1 1
 SQ SEQUENCE 1074 AA; 117623 MW; 72B32E37D00382E4 CRC64;

Query Match	66.3%	Score 350;	DB 2;	Length 1074;
Best Local Similarity	60.4%	Pred. No. 3e-27;		
Matches	61;	Conservative 18;	Mismatches 22;	Indels 0;
			Gaps	0

[illegible]

Db 412 NGNCVLGHTHADVYQMQLPVPVNYNLTLCRGYPLPDDSE 452

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